Add11885 Artibody
Add1702 Modified
Ady79579 Chimeric
Ady92239 Human bon
Ady84096 Eartial a
Ady83157 Gangliosi
Ady93704 The kappa
Ady93704 The kappa
Ady93701 Humanised
Adh4591 O23 light
Adw65810 Humanised
Add14591 O23 light
Add87940 Anti-IFN-Ads97940 Anti-IFN-Ads97940 Anti-IFN-Ads97940 Anti-IFN-Ads9437 Anti-IFN-

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OM protein

Run on:

Sequence:

Searched:

Database

Result

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Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour; cancer; therapy; mutant; mutein.
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93. .100
/label= CDR3
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/note= "framework region 2"
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101. 131
/label= FR4
ABJ38595
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AAY92239
AAX92239
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/label= CDR2
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/label= CDR1
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/label= FR3
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/label= FR1
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     Misc-difference
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AAB20358
       Aab20358 Anti-chel
Aab20369 Anti-chel
Aad20360 Anti-chel
Adq38051 Chimeric
Adq38051 Chimeric
Adx23362 Human CD7
Aav82740 Plasmid p
Aab82834 Antibody
Aab82847 Antibody
Aab82847 Antibody
Aab82834 Antibody
Aab8285 A Gimeric
Aab80025 A Gimeric
Aab80025 A Gimeric
Aab80025 A Gimeric
Aab80031 Human mon
Adf65776 Human mon
Adj92516 Human soJ
Aac34878 BIWA4/8 a
Adl15445 Humanised
Aac35326 Humanised
Aac35326 Humanised
Aac35326 Humanised
Aac360849 Humanised
Aac36878 Humanised
Aac36878 Humanised
Aac36878 Humanised
Aac3688 Humanised
                                                                                                                          7, 2005, 15:28:46; Search time 114.5 Seconds (without alignments) 736.365 Million cell updates/sec
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                                                                                                                                                                                                                 1132
1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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ADQ31891
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ADQ98050
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AAE34877
ADL15441
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Gapop 10.0 , Gapext 0.5
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11: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp201s:*
6: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
                                                                                             protein search, using
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Maximum DB seq length: 2000000000
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                       /note= "encoded by TYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 12; 100pp; English
                                                                                                                                                                                                    27-SEP-1999; 99US-0156194P.
31-MAY-2000; 2000US-0208684P.
                                                                                                                                                          27-SEP-2000; 2000WO-US026619
                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                Chmura A;
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Misc-difference 207
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                                                                 WO200122922-A2
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Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
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                                                                              engineering; metal chelate; CHA255; indium; EDTA; tumour;
                                                                                                                                                                                              "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                        'note= "complementarity determining region 3"
                                                                                                                                                                                                                                                           "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                     101. .131
/label= FR4
/note= "framework region 4"
                                                                                                                                                                 "framework region 1"
                                                                                                                                                                                                                             "framework region 2"
                                                                                                                                                                                                                                                                               /label= FR3
/note= "framework region 3"
                                                           Anti-chelate antibody CHA255 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "encoded by AGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            by TYG"
                                                                                                                                                                                                                                                                                                                                                                                                                  by ACK"
                                                                                                                                 ocation/Qualifiers
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AAB20359 standard; protein; 218
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31-MAY-2000; 2000US-0208684P.
                                                                                                                                                                                                       38. .52
/label= FR2
                                                                                                                                                                                                                                                'label= CDR2
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|abel= CDR3
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/label= CDR1
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|abel= FR1
                                       (first entry)
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                                                                                          cancer; therapy
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                                                                                                              Mus musculus,
                                       11-JUN-2001
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                    AAB20359;
                                                                                Antibody
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complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The reactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain of antification. The present sequence is that of the light chain of antification of antibody CHA255. As an example of the method of the invention, rational computer-aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable could be expressed in Escherichia coli, and the synthesis and screening of benzyl-EDTA chelates carrying weekly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A reactive site was innorporated into the antibody by engineering a late of the antibody to which the chelate bound. This was accomplished by site-directed mitagenesis of a nucleic acid consists the conjugation of the conjugation of the antibody to which the chelate bound.
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                                                                                                                                                                                                                                                                                                                                                                   encoding the wild-type of the anti-chelate antibody
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/label= CDR2
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/label= CDR1
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Best Local Similarity 99.5'
Matches 217; Conservative
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/label= 1
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 218 AA;
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The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The reactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond: The present sequence is that of the light chain variable covalent bond: The present sequence is that of the light chain variable region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C mutation. As an example of the method of the invention, rational computer region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C covalently to CHA255 bound to a tumour and then to covalently or CHA255 bound to a tumour and then to covalently or CHA255 bound to a tumour and then to covalently attach the covalently to CHA255 bound to a tumour and then to covalently attach the channer of the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a covalently actorphilic groups capable of conjugation of the antibody in covic. This Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Abn.96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site conficed mutagenesis of a nucleic acid encoding the wild-type of the conficed mutagenesis of a nucleic acid encoding the wild-type of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
                                                   93. .100
/label= CDR3
/note= "complementarity determining region 3"
                                                                                                                         note= "replaces Ser of wild-type sequence"
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                                 'note= "framework region 3"
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/label= FR4
/note= "framework region
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31-MAY-2000; 2000US-0208684P.
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               'label= FR3
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                                                                                                                                                                                                                                            Misc-difference 112
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                                                                                                            Misc-difference 95
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Score 1113; DB 4; Length 218; Pred. No. 1.6e-78;

98.3%;

Query Match Best Local Similarity

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                                                                                          VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                                              121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                           VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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                                                                                                                                                                                                                                                                                                                                                       Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                      1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                        RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                                                                                                               I F P S D E Q L K S G T A S V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S
                                                                                                                                                                                                                                                                                                                                                                              murine; mouse; chimeric; human; TTCL; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography.
Gaps
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2; Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                          ADQ98050 standard; protein; 218 AA
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22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631259.
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216; Conservative
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N-PSDB; ADQ98054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
Chimeric.
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Matches
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ADQ98050
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                describes using these antibodies for in vivo imaging where the antibody comprises a targeting molety that binds specifically to a cell via a cell surface receptor or antigen thus forming a cell-autant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex. Is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminascence, gamma-emissions or single photon emission tomography (SPFT). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit typestic and immunosuppressive activities. This polypeptide sequence is the chimeric murine antibody 2D12.5 variable light chain protein fused to the human anti-tetanus toxin antibody kappa light chain constant region
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reactive functional group of the metal chelate. The present invention
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22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.9
Matches 209, Conservative
                                                                                                                                                                                                                                                                                                                                                                          of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004065569-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ98051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
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chelating agents and metal chelates, particularly macrocyclic metal chelates. Specifically, it refers to an antibody that comprises a metal chelates. Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate che as a reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a naturally occurring amino acid e.g. the -SH group side chain of a cysteine residue (not present in the wild type) which can be used to form a covalent bond between the reactive site of the antibody and the cactive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody complex. On addition of the metal chalate forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide sequence is the chimeric mutant N33C murine antibody 2D12.5 variable light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                                                                                        Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                                                                                                                                                                                                                                                                                invention relates to multi-functional antibodies that recognise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, CD72, B-lymphocyte; receptor; scFv; antibody; cytostatic; immunosuppressive; cancer; autoimmune disease; gene therapy.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 95.2%; Score 1078; DB 8; Length 218; Local Similarity 95.9%; Pred. No. 8.2e-76; nes 209; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                      Claim 41; SEQ ID NO 28; 208pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CD72-targeted IgG1 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constant region of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR23362 standard; protein; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-2004 (first entry)
(REGC ) UNIV CALIFORNIA
                                      Corneillie
                                                                            WPI; 2004-580725/56.
N-PSDB; ADQ98055.
                                                                                                                                                                                                             autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR23362;
                                        Meares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR23362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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9

Gaps

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The present sequence is the protein sequence of the light chain of human CC 1gd1 antibody 025, which specifically recognises human B cell associated antigen CD72. An scrv ADR23124 selected from an antibody phage display library was shown to specifically recognise the human CD72 receptor. The scrv was recloned in IgG expression vector C01 using primars designed to scrv was recloned in IgG expression vector C01 using primars designed to scrv was recloned in IgG expression vector C01 using primars designed to scrv restore complete human frameworks, thereby generating antibody 025. Such anti-CD72 immunosolobulins or their antigen-binding fragments can be used as internalising human binding molecules are capable of (specifically) binding to CD72 or its antigenic determinant, and preferably bind to CD72 casque with cells. Upon binding to CD72 present on the surface of target cells, the binding molecules internalise. In addition to the internalising human binding molecules, the invention provides of target cells, the binding molecules, the invention provides of carget cells, the binding molecules, the invention provides of the internalising human binding molecules, immunoconjugates, nucleic acids encoding these, and compositions comprising them. The internalising human binding molecule, immunoconjugates, nucleic acids encoding these, and compositions comprising them. The molecule or composition can be used in the diagnosis and/or treatment of molecule and B cell associated disorder or disease, especially a B cell associated autoimmune disorder (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARPSGSLIGDKAALTITGAQTEDEARYFCALWYSC--LWVFGGGTKLTVLSRTVAAPSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SAVVIQESALITISPGETVILICRSSIGAVITISNYANWVQEKPDHLFTGLIGGINNRAPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.6%; Score 776; DB 8; 73.5%; Pred. No. 2.4e-52; iive 16; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; SEQ ID NO 54; 174pp; English
                                      Location/Qualifiers
                                                    1. .109
/label= V_region
110. .215
/label= C_region
                                                                                                                                                                                                                                          27-JAN-2003; 2003WO-EP050004.
                                                                                                                                                                                                                                                                                 27-JAN-2003; 2003WO-EP050004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                         (CRUC-) CRUCELL HOLLAND
                                                                                                                                                                                                                                                                                                                                                                   Bakker ABH, Marissen
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-580978/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADR23361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 215 AA;
                                                                                                                                                            WO2004067569-A1.
Homo sapiens.
                                                                                                                                                                                                    12-AUG-2004.
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                                        Key
Region
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SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is used in a method for obtaining a novel gene construct (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-targeting group (I) and a heterologous prodrug-converting enzyme (II), and (B) is directed to leave the cell for selective localisation at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target site, then administration of (III) is used for targeted release of cytocoxic drug, specifically for treating cancer but also inflammation such as rheumatoid arthritis. In situ generation of the targeting antibody increases selectivity, reducing side effects at normal tissue. The method is applicable to any antibody-directed enzyme prodrug therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New gene construct expressing conjugate of targetting agent and prodrug-converting enzyme - useful for, e.g. targetted production of cytotoxic drug in vivo, especially for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VVTQESA-LITSPGETVTLICRSSIGAVTISNYANWVOEKPDHLFTGLIGGINNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLSQSPAILSASPGEKVTMTCRAS----SSVTYIHWYQQKPGSSPKSWIYATSNLASGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       Conjugate; cell targeting; cytotoxic drug; prodrug therapy system; prodrug-converting enzyme; cell surface antigen; treatment; cancer; inflammation; rheumatoid arthritis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                  Plasmid pNG3/A5B7VK-HuCK-NEO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1f; Page 70; 100pp; English.
AAW82740 standard; protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-GB001294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97GB-00009421
                                                                                                             (first entry)
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Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blakey DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-059700/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV72047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 235 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-1997;
                                                                                                             10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-1998
                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emery SC,
                                                     AAW82740;
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RESULT

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The present invention relates to domain deleted CC49 or C2B8 antibodies. Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CH2 domain has been deleted and are reactive with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2B8 construct where the CH2 domain has been deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel domain deleted CC49 antibody reactive with tumor associated antigen -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from neoplastic disorder such as haematologic neoplasm, preferably non-Hodgkin's lymphoma. Autibodies of the invention are also used to treat neoplastic disorder, colon cancer and haematologic malignancy. They are useful for reducing tummour size, inhibiting tummour growth and/or prolonging the survival time of tumour-baring animals and for treating tummours. The present sequence is human C2B8 light chain protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                  Human, CC49 antibody, C2B8 antibody, tumour associated antigen, TAG-72, neoplasm, neoplastic disorder, haematologic neoplasm, colon cancer, non-Hodgkin's lymphoma, haematologic malignancy, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 VFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RSAVVIQES -- ALTISPGETVILICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 755.5; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 1e-50;
16; Mismatches 42;
                                                                                                                                   Human C2B8 antibody light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 3B; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chinn
                     AAE27925 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
                                                                                                                                                                                                                                                                                                                                                            29-JAN-2002; 2002WO-US002373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.5%;
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Braslawsky GR, Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-698547/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD45754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 235 AA;
                                                                                                                                                                                                                                                                                   WO200260955-A2.
                                                                                             27-DEC-2002
                                                                                                                                                                                                                                                                                                                        08-AUG-2002
                                                          AAE27925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
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PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antiinflammatory; cardiovascular; gene therapy; antibody; Fc; agriculture; industrial application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antibody comprising an Fc variant portion having an amino acid modification in the Fc region of the parent Fc polypeptide, where the Fc variant modulates binding to an Fc-gamma-R compared to the parent Fc polypeptide. The antibody may also be used in research and in agricultural or industrial applications. This sequence corresponds to the light chain of the antibody "Rituximab" as an example of an antibody of the invention.
VFIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New optimized Fc variant antibody useful for diagnosing or treating diseases (e.g. cancer, inflammation or cardiovascular diseases), in research and in agricultural or industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Indels
                                                            LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                             Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 755; DB 8, 71.8%; Pred. No. 1e-50; iive 16; Mismatches
                                                                                                                                                                                                                                                          Antibody "Rituximab" light chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 12; Fig 31a; 192pp; English.
                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Dang W,
Vafa O;
                                                                                                                                                                   ADL92471 standard; protein; 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2002; 2002US-0414433P.
23-JAN-2003; 2003US-0442301P.
02-MAY-2003; 2003US-0467666P.
12-JUN-2003; 2003US-0477839P.
                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2003; 2003WO-US030249.
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chirino AJ,
Karki SB, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-316096/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 213 AA;
                                                                                                                                                                                                                                                                                                                                                                 WO2004029207-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (XENC-) XENCOR
                                                                                                                                                                                                                              01-JUL-2004
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
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                                                                                                                                                                                                  ADL92471;
       119
                                                                                           196
                                                               179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Науев
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lazar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                         RESULT 10
                                                                                                                                                        ADL9247
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                                                                 à
                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a dimeric antibody (I) comprising several moromeric subunits, where the monomeric subunits are non-covalently associated. (I) is useful for treating a disorder, especially immune disorder, and neoplastic disorder such as relapsed Hodgkin's disease, resistant Hodgkin's disease high grade, low grade and intermediate grade non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia B-CLL), lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), diffuse large cell chronic cell lymphoma (MCL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma, AIDS-related lymphoma, manorytic B cell lymphoma, angloimmunoblastic lymphoma, and loiaved cell, large cell immunoblastic lymphoblastoma, small, non-cleaved burkitt's and non-Burkitt's, follicular, mixed small cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a detailed description of the various uses of (I)). The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel dimeric antibody useful for treating immune disorder and neoplastic disorder, has several non-covalently associated monomeric subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                               C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic; veotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic; thyromimetic; heparotropic; heamostatic; antileprotic; antibacterial; neuroprotective; antipsorialic; antirheumatic; antiarthritic; antiuloer; dermatological; immunosuppressive; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 RGQIVLSQSPAILSASPGEKVTWTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
       LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 755.5; DB
Pred. No. 1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hariharan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۵,
                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3B; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chinn
                                                                                    ABB82834 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
21-DEC-2001; 2001US-0341858P.
                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002; 2002WO-US002374.
                                                                                                                                             (first entry)
                                                                                                                                                                         Antibody C2B8 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Braslawsky GR, Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-140446/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABZ24018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                            WO200296948-A2
                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                            31-MAR-2003
                                                                                                                                                                                                                                                                                                                                                         05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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          196
                                                                                                                ABB82834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                        RESULT
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Doberstein SK;

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122 117

(revised)
(first entry)

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AAB08025 standard; protein; 235 AA.
                                                   12-SEP-2003
14-NOV-2000
                                   AAB08025;
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                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                Peptide
RESULT 12
AAB08025
                                                                                                                                                                                     Mus
                  7
                                                                                                                                                                                                                                                                                                                                                                         5D5 Fab comprises a light chain (AAW07528) and heavy chain (AAW07529) of monoclonal antibody (MAD) 5D5, a murine MAD raised against the hepatocyte growth factor (HGF) receptor (c-Met). The Fab can be obtd. by papain digestion of the MAD or by recombinant methods utilising cDNA clones (AAAT41873-74) coding for the light and heavy chains. 5D5 Fab is an antagonist of the HGF receptor and is useful for the diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                     Hepatocyte growth factor receptor antagonist - specifically anti-c-Met receptor monoclonal antibody 5DS Fab, useful for mammalian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALTISPGETVILICRSSIGAVITS --- NYANWVQEKPDHLFTGLIGGINNRAPGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                Hepatocyte growth factor receptor; HGF; c-Met, antagonist; monoclonal antibody; MAb; Fab; breast cancer; pancreas cancer; colon cancer; lung cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of breast, pancreas, colon and lung cancer
          LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.3%; Score 751; DB 2; 71.8%; Pred. No. 2.1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKADYERHKVYACEVTHQGLSSPVTKSFNRGEC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                Anti-HGF receptor MAb 5D5 Fab light chain.
                                                            AAW07528 standard; protein; 220 AA
                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig 1A; 69pp; English.
                                                                                                                                                                                                                        96WO-US008094.
                                                                                                                                                                                                                                        95US-00460368.
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                           Tabor KH;
                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                             WPI; 1997-034371/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     N-PSDB; AAT43873.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 220 AA;
                                                                                                                                                                                    WO9638557-A1
                                                                                                                                                                                                                       31-MAY-1996;
                                                                                                                                                                                                                                        02-JUN-1995;
                                                                                              04-MAR-1997
                                                                                                                                                                                                       05-DEC-1996.
                                                                                                                                                                                                                                                                           Schwall RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 153;
                                                                                                                                                                                                                                                                                                                                        treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
183
                178
                                                                             AAW07528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128
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                                                                                                                                                                   Mus sp.
                                           RESULT 11
                                                   AAW07526
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The present sequence represents a dimeric anti-CD20 light chain

CC polypeptide. The dimeric immunoglobulin is used in the method of the
polypeptide. The dimeric immunoglobulin is used in the method of the

CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
cengineering a monoclonal antibody to introduce a cysteine molecule which

CC endineer that is capable of activating components of the complement

CC heavy chains on the same antibody molecule. The dimer is a homodimer or

CC heavy chains on the ability to activate and kill cells via the complement

CC cascade. The dimer is also capable of binding to Fegamma receptors on

CYCLOXIC effector cells and on host immune cells, and is capable of

initiating programmed cell death. The IgG/IgG dimers may be used to treat

CC anterdic disorders, cancers and autoimmune diseases such as allergic

atopic dermatitis, Crohn's disease, Graves's disease, food allergies,

CC allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They

may also be used to treat a range of other diseases and disorders such as

crhemmatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's

disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis
                                                               Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG; complement system; Fcgamma receptor; cytotoxic effector cell; host immune cell; altestic disorder; cancer; autoimmune disease; allergic asthma; altopic dermatitis; Crohn's disease; allergic asthma; atopic dermatitis; Crohn's disease; allergic bronchopulmonary aspergillosis; allergic rhinitis; Graves's disease; food allergy; allergic contact dermatitis; cancer; B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis; pigeon breeder's disease; hepatitis; leprosy; Lyme disease; disease; aplastic anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetically engineering immunoglobulin (Ig) G/IgG dimers for the treatment of cancers, allergic disorders and autoimmune conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129. .215
/note= "human kappa light chain constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hariharan K, Labarre MJ, Huynh TB;
A dimeric anti-CD20 light chain polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1A-B; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IDEC-) IDEC PHARM CORP.
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Chimeric.
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and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected cell populations. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human rabies-immune globulin; monoclonal; virucide; heavy chain; monoclonal rabies virus neutralising antibody; immunoglobulin; chain; central nervous system; CNS; prophylactic therapy; clone JA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating an individual exposed to a rabies virus by administering to the
                                                                                                                                                           28
                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the light chain protein of the monoclonal antibody from clone JA. The invention relates to an isolated human monoclonal rables virus neutralising antibody (virucide) derived from cDNA clones encoding the antibody heavy and light chains expressed in heterologous expression systems and purified away from deleterious contaminants. The invention provides a fused gene encoding a chimeric immunoglobulin light chain and a fused gene encoding a chimeric immunoglobulin heavy chain. The antibody of the invention is useful for
                                                                                                                                                                                                                                                                                     119 VPIFPPSDEQLKSGTASVVCLLANPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
                                                                                                                                                                                                                                           136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
                                                                                                                                                           1 RSAVVIQES--ALTISPGETVTLICRSSIGAVITSNYANWVQEKPDHLFIGLIGGINNRA
                                                                                                                                                                             21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKRWIYATSNLA
                                                                                                                                                                                                                       59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human monoclonal rabies virus neutralizing antibody for treating individual exposed to rabies virus and for preventing of rabies virus to central nervous system.
                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain protein of the monoclonal antibody from clone JA.
                                                                                                Length 235;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                   LSSTLTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                DB 3;
                                                                                             66.3%; Score 750.5; DB 3 70.0%; Pred. No. 2.5e-50;
                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 24-25; 25pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO14066 standard; protein; 234
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                                                                                                                  Best Local Similarity 70.0
Matches 154; Conservative
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N-PSDB; AAK98702.
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                                                                                                  Query Match
Best Local Similarity
                                                                    Sequence 235 AA;
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individual a therapeutically effective amount of the antibody, and preventing a spread of the rabies virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious post-exposure prophylactic therapy for individuals exposed to a rabies virus
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                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                       The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable region. Rabies is an acute, neurological disease caused by infection of the central nervous system with the rabies virus, a member of the Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant expression vector comprising the nucleic acid
                                                                                                                                                                62
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                                                                                                                                                                                  PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                                          ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; constant region; monoclonal antibody 57, Mab 57 variable region; Rabies; neurological disease; infection; central nervous system; rabies virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; light chain.
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                                                                                                      Length 234;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                               218
                                                                                                      66.2%; Score 749.5; DB 5; 71.8%; Pred. No. 3e-50; ive 13; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                           234
                                                                                                                                                                                                                                                                                                                                                                LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 33-34; 38pp; English
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                                                                                                                        Best Local Similarity /1.81
Matches 155; Conservative
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                                                                             Sequence 234 AA;
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                                                                                                          Query Match
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molecule encoding the antibody, and isolating the recombinant antibody expressed and treating an individual exposed to a pathogen by administering to the individual the recombinant antibody. The recombinant antibodies are useful for preventing (vaccine) and treating an individual exposed to a pathogen, e.g. rabies infection. They are also useful for the qualitative and quantitative determination of the rabies virus. The sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
                                                                                                                                                                                                                                                                                               ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                            ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138
                                                                                                                                                                                                                                                                                                                                                                          PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198
                                                                                                                                                                                                                                                                VLTOSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79
                                                                                                                                                                                                                                      4 VVTQESA-LITSPGETVTLICRSSIGAVTISNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                                                                                                                                                                                           Gaps
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monoclonal rabies virus neutralising antibody; rabies virus protein;
neuronal tissue; antirabies.
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                                                                                                                                                                            Length 234;
                                                                                                                                                                                                           Indels
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                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                    LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                                                                            Score 749.5; DB Pred. No. 3e-50;
                                                                                                                                                                  66.2%; Scur.
71.8%; Pred. No. 3c.
71.8%; Mismatches
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04-MAY-2001; 2001US-00848832.
21-AUG-2001; 2001US-0314023P.
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N-PSDB; ADF65790.
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DIETZSCHOLD
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                       expression vector
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                                                                                                                                                  Seguence 234 AA;
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rch completed: June time : 117.5 secs

Search

New isolated nucleic acid molecule encoding a sequence that neutralizes an antibody that binds to rables virus protein, useful for diagnosing, preventing or treating infection of pathogens that target neuronal tissues, e.g. rabies.

Claim 2; SEQ ID NO 4; 22pp; English

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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of immunoglobulin (Ig) heavy and light chains of human monoclonal rabies virus neutralising antibody, and the polynucleotide sequences encoding them. The antibody specifically binds to a rabies virus protein. Also disclosed is a fused gene encoding a chimeric immunoglobulin light or heavy chain comprising first DNA sequence encoding an immunoglobulin light or heavy chain variable region of a monoclonal rabies virus neutralising antibody produced by a heterohybridoma cell line and a second DNA sequence encoding a recombinant antibody. The polynucleotide sequences, antibodies and methods are useful for diagnosing, preventing or treating an infection of pathogens that target neuronal tissues, particularly realism.
                                                                                                                                                                                                                                                                                                                                                                                                                 79
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                            Sequence 234 AA;
                                                                                                                                                                                                                                                                                                                                             Matches 155;
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Sequence Sequence Sequence Sequence

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Run on:

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ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.0%; Score 759; DB 3; Length 235; Best Local Similarity 72.2%; Pred. No. 1.6e-67; Matches 156; Conservative 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.; STREET: 1100 New York Ave., N.W.
CITY: Washington STATE: D.C.
COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MADDIUM FYPE: Floppy disk
        US-09-466-635-4
US-08-630-820-6
US-08-273-453-6
US-08-127-101A-5
US-09-027-449-72
US-09-026-985-72
US-09-121-952A-72
US-09-234-340A-72
US-09-627-896-85-22
US-09-027-896-85-6
US-09-121-952A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIPICATION NUMBER: US/09/10-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 10-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; STRANDEDMESS: single; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-423-439-18
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RESULT 1
US-09-423-439-18
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                                                                                        7, 2005, 15:42:01; Search time 29.5 Seconds (without alignments) 551.644 Million cell updates/sec
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                                                                                                                                                                     1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218
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Sequence 6
Sequence 2
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'cgn2_6/ptodata1/iaa/5A_COMB.pep:*
'cgn2_6/ptodata1/iaa/5B_COMB.pep:*
'cgn2_6/ptodata1/iaa/6A_COMB.pep:*
'cgn2_6/ptodata1/iaa/6B_COMB.pep:*
'cgn2_6/ptodata1/iaa/BECOMB.pep:*
'cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-952-235-1

US-09-669-971-1

US-09-472-087-67

US-09-472-087-67

US-09-011-769A-27

US-08-315-926A-79

US-09-472-087-14

US-09-472-087-14

US-09-472-087-14

US-09-472-087-14

US-09-472-087-17

US-09-453-234-46

US-09-453-234-46

US-09-453-234-46

US-09-453-234-46

US-09-456-090A-36

US-09-456-090A-36
                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                  protein search, using sw model
                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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1132
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Match Length
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Minimum DB Maximum DB

Database

Result Š

Searched:

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**Gaps** 

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RESULT 3
JS-09-669-971-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
81 ARFSGSGSTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139
                                    PPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                     140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Indels
                                                                                                            LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                               LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.3%; Score 751; DB 3; 71.8%; Pred. No. 9.2e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/952,235
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marsechang, Diane L.
REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,
                                                                                                                                                                                                                                    Sequence 1, Application US/08952235 Patent No. 6207152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P09:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 220 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.8<sup>3</sup>
Matches 153; Conservative
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US-08-952-235-1
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69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.3%; Score 751; DB 4; Length 220; Best Local Similarity 71.8%; Pred. No. 9.2e-67; Matches 153; Conservative 14; Mismatches 42; Indels
                                                                               APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-Jul-2001
CLASSIFICATION: CURROWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/460368
FILING DATE: 02-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Marschang, Diane L.
REGISTRATION UNDBR: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 15, Application US/09472087; Patent No. 6682736
; Sequence 1, Application US/09669971; Patent No. 6468529
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 220 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                STREET: 1 DNA Way
                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-472-087-15
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123 PPSDEQLKSGTASYVCLLANNYYPREAKVOWKVDNALOSGNSOESVTEODSKDSTYSLSST 182
                                                                                                                                                                           4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                        63 ARFSGSLIGDKAALTITGAQTEDEARYFCALMYSCLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.2%; Score 738; DB 4; Length 235; 71.3%; Pred. No. 2e-65; tive 15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pillsbury Madison & Sutro, LLP
                                                                                                                                                                                                                                    183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HENNEQUIN, Laurent F.A.
MARSHAM, Peter R.
DOWALL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

CONDITRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 New York Ave., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09011769A Patent No. 6436691 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-AUG-1995 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Anthony M.
David C.
David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 235 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  John F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 71.3
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLAKEY,
DAVIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SLATER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HENNAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-011-769A-27
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US-09-011-769A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VVTQE-SALITSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANNE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPERENCE: ABX.-PF.
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 67
LENGTH: 233
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                      APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVEREY
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI.
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.4%; Score 740; DB 4; Length 233; Best Local Similarity 70.4%; Pred. No. 1.2e-65; Matches 152; Conservative 18; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Patent No. 6682736
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     CRGANISM: Homo sapiens US-09-472-087-15
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US-09-472-087-67
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Best Local Simil
Matches 152;
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 15
LENGTH: 233
TYPE: PRT
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Sequence 79, Application US/09315926A

Sequence 79, Application US/09315926A

Batent No. 6498027

GENERAL INFORMATION:
APPLICANT: BE VAIN. Helmuth
APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
FILE REFERENCE: 2183 4080US
CURRENT APPLICATION NUMBER: US/09/315,926A
CURRENT APPLICATION NUMBER: EP 99201593.3
PRIOR FILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SCOFTWARE: PatentIn version 3.0
SEQ ID NO 79
LENGTH: 236
119 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 RPSGSGSGTDYTLTISSLQPEDPATYYCQQYSTVPWTFGQGTKVEI-KRTVAAPSVFIFP 142
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                                                                                                                                              119 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
HEADLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REPERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Sequence is synthesized; Patent No. 6828121
US-10-011-125A-2
                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/10011125A; Patent No. 6828121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                          US-10-011-125A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 491
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   ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                         SRFSGSGSGTDYTLTISSLQPEDIATYYCQHWSSKPPTFGQGTKVEV-KRTVAAAPSVFIF 139
                                                                                                                                       PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                             140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WS-08-397-411-12

Sequence 12, Application US/08397411

Sequence 12, Application US/08397411

Sequence 10. 6129914

GENERAL INFORMATION:

APPLICANT: Gingrich, Roger

APPLICANT: Link, Brian

TITLE OF INVENTION: Bispecific Antibody Effective to Treat

TITLE OF INVENTION: B-6-11 Lymphoma and Cell Line

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 213;
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MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/397,411

FILING DATE: 01-MAR-1995

CLASSIFICATION: 424

PRICH PATE TO MAREN: US 07/859,583

FILING DATE: 27-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGIGTRATION NUMBER: 30,223

REGISTRATION NUMBER: 011823-004901

TELEFPHONE: 415-326-2400

TELEFPAN: 415-326-2400

TELEFPAN: 415-326-2400

TELEFRAN: 415-326-3400

TELEFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 213 amino acids
amino acid
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STATE: California
COUNTRY: USA
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Best Local Similarity
Matches 152; Conserv
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140 PPSDEQLKSGTASVVCLLANFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VVTQE-SALTISPGETVTLICRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 71, Application US/09472087

| Sequence 71, Application US/09472087
| Patent No. 6682736
| GENERAL INFORMATION:
| APPLICANT: HANSON, DOUGLAS C. APPLICANT: HANSON, MARK J. APPLICANT: HANKE, IELLEN E. APPLICANT: HANKE, JEFFREY H. APPLICANT: DAVIS, C. GEOFFREY C. APPLICANT: DAVIS, C. GEOFFREY C. APPLICANT: CORVALAN, JOSE R. TITLE OF INVANTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4 FILE REPERBNCE: ASV-PP1 CURRENT FILING DATE: 1999-12-23 PRIOR PPLICATION NUMBER: 60/113,647
| PRIOR PPLICATION NUMBER: 60/113,647
| RICHER REPERBNCE: ASP PP1 CURRENT FILING DATE: 1999-12-23 NUMBER OF SEQ ID NOS: 147
| SOFTWARE: PATENTING VET. 2.1
                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NUTLER, ELLLEN E.
APPLICANT: MUELLER, ELLLEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVALIAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PPI
CURRENT APPLICANT: 1999-12-23
PRIOR PILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATCHIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.7%; Score 732; DB 4; Length 235; 69.4%; Pred. No. 7.8e-65;
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200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
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                                                                                                         Sequence 65, Application US/09472087
Patent No. 6682736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                 RESULT 11
US-09-472-087-65
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LENGTH: 214
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                                                                                                                                                                                                                                                                                                                                                   GDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPSDEQLK 130
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                                                                                                                                                                                                                                                                                         11 LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGSLI
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Sequence 14, Application US/09472087

Batent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: MUELLER, EILLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: GORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1

CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT PILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

SOFTWARE: PATENTION TOWNER: 60/113,647

SOFTWARE: PATENTION VOINGER: 1098-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATENTIN VET. 2.1

SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.7%; Score 732; DB 4; Length 235; ilarity 69.4%; Pred. No. 7.8e-65; Conservative 19; Mismatches 43; Indels
                             NAME/KEY: misc feature
OTHER INFORMATION: Description of Artificial Sequence: phage
NAME/KEY: PEPTIDE
                                                                                                                                                                             Length 236;
                                                                                                                                                                               Query Match 64.8%; Score 734; UB 4; Lemyun 2. Best Local Similarity 72.6%; Pred. No. 4.98-65; Matches 151; Conservative 13; Mismatches 42; Indels
                                                                              ; LOCATION: (1)..(236)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79
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Best Local Simi
Matches 150;
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Query Match

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63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 224;
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| Sequence 17, Application US/09472087
| Patent No. 668236
| GENERAL INFORMATION:
| APPLICANT: HANSON, DOUGLAS C. |
| APPLICANT: HANSON, DOUGLAS C. |
| APPLICANT: HANKE, IELEN E. |
| APPLICANT: HANKE, JEFFREY H. |
| APPLICANT: HANKE, JEFFREY H. |
| APPLICANT: GILANN, STEVEN C. |
| APPLICANT: DAVIS, C. GEOFFREY H. |
| APPLICANT: CORVALAN, JOSE R. |
| TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4 |
| FILE REFERENCE: ASE FFI. |
| CURRENT APPLICATION NUMBER: US/09/472,087 |
| CURRENT FILING DATE: 1999-12-23 |
| PRIOR FILING DATE: 1999-12-3 |
| NUMBER OF SEQ ID NOS: 147 |
| SEQ ID NO 17 |
| LENGTHREE PATENTION VET. 2.1 |
| SEQ ID NO 17 |
| TURNER IN THE PATENTION OF 
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                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SENGTH: 224
Valkirs, Gunars
Gray, Jeff
Lonberg, Nils
Biosite Diagnostics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
COTHER INFORMATION: M2-32L
US-09-453-234-84
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US-09-472-087-17
                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPFTFGPGTKVEI-KRTVAAPSVFIFP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
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                                                                                                                                                                                                                    5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
                                                                                                                                                                                                                                                       3 VLTÓSPATLSLSPGERATLSCRAS---QSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIP 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 214;
                                                                                      64.5%; Score 730.5; DB 4; Length 69.8%; Pred. No. 9.7e-65; ive 20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                      Best Local Similarity 69.89
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 71.2
Matches 153; Conservative
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US-09-456-090A-84
; ORGANISM: Homo sapiens
US-09-472-087-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-456-090A-84
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US-09-453-234-84
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Query Match

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7, 2005, 16:00:22 ; Search time 100 Seconds (without alignments) 785.243 Million cell updates/sec
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1132
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 27, Appl Sequence 28, Appl	Sequence 42, Appl Sequence 1, Appli	Sequence 1, Appli	4.	Sequence 2, Appli Sequence 8, Appli	8	Sequence 8, Appli	Sequence 4, Appli
SUMMARIES	US-10-625-047-27 US-10-625-047-28	US-10-723-003-42 US-09-995-693-1	US-10-232-408-1	US-10-225-108A-4	US-10-461-148-2 US-10-150-475A-8	US-10-704-522-8	US-10-645-215-8	US-10-150-475A-4
DB	16 16	16	4.5	17	14	16	16	14
% Query Match Length DB	218	235	220	234	234 213	213	213	213
% Query Match	95.3	66.7	66.3	99	66.2 66.2	66.2	66.2	0.99
Score	1079	755.5	751	749.5	749.5	749	749	747
Result No.	4.0	W 4	ינחע	7	დთ	10	11	12

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95.3%; Score 1079; DB 16; Length 218; llarity 95.9%; Pred. No. 1.8e-83; Conservative 0; Mismatches 9; Indels 0

Best Local Similarity Matches 209; Conserv

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US-10-625-047-27 Query Match PERTURE: OTHER INFORMATION: Description of Artificial Sequence:native cloned OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody OTHER INFORMATION: kappa light chain constant region (TTCL)

SEQ ID NO 27 LENGTH: 218 TYPE: PRT ORGANISM: Aṛtificial Sequence

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	14	747	φ	213	16	-10-645-215-4	equence 4,	
	12	742	9	215	12	-10-307-724-12	eguence 122,	
	16	742		215	16	US-10-737-290-122	122	
	17	742		239	16	14	142,	
	ά.	741		213	5	12	12,	
	9 6	740		233	7	US-10-153-382-11	11,	
	1 6		3 4	000		115-10-612-497-15	'n.	
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	25	738.5	65	234		US-IU-U45-6/4-58/	Sequence 30', App	
	26	737	65	215		US-10-128-520-106	Sequence 106, App	
,	27	736.5	65.1	234	12	US-10-292-088-88	Sequence 86, Appl	
,	28	735.5	92	214		US-IO-364-953-I	Sequence 1, Appli	
j j	53	735.5	65	237		US-10-020-786-10	sequence to, Appr	
	30	735.5	65	667		US-10-764-428-7		
	31	735.5		667		US-10-764-428-13		
	32	735.5	. 65	667		US-10-764-428-25	Sequence 25, Appl	
:	33	735.5	65	670		US-10-764-428-5	Sequence 5, Appli	
	34	735.5	65.	670		US-10-764-428-9	Sequence 9, Appli	
	35	735.5	65	670		US-10-764-428-11	ednence	
	36	735.5	65.	670		US-10-764-428-27	27,	
	37	735	64.	235		US-10-656-769-38	e 38	
	38	734.5	64.	237	6	US-09-056-160B-100	100	
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	US-10-6	US-10-625-047-27	27					
	; Seque	nce 27,	Sequence 27, Application US/10625047	tion US	/106	25047		
	; Publi	cation	No. US20	0401989	62A1			
	; GENER	AL INFO	RMATION:					
	; APPL	ICANT:	APPLICANT: Meares, Claude	Claude				
	; APPL	ICANT:	Cornell	lie, To	g			
		ICANT	The Rec	lents of	Ĕ,	APPLICANT: The Regents of the University of California		
	, TITL	NI GE	VENTION:	Multi-	Ĭ.	tional Antibodies		
	, FILE	REFERE	NCE: UZ:	12000	1	(10 / 10 / 10 / 10 / 10 / 10 / 10 / 10 /		
	CURR CURR	ENT APP	TAICALLO	NOMBER	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	CURRENT APPLICATION NUMBER: US/IO/025,04/		
	, CURK	ENT FIL	TING DAIL	. ממממאות		0/3E0 EEE		
	, PRIC	A APPLI	PRIOR APPLICATION NUMBER: US IN/350, DRIOD DILING DATE: 2003-01-23	2003-01	3,5	n		
	, FRIC	NTTT 1 20	MINDED OF SEC IN NOS	20.20	3			
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	SEO ID NO	`	מרכוורדיי	4	4			

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VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
                         121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                                                                121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: N53C cloned OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 42, Application US/10723003
Publication No. US20040254108A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: G40, Yajun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE FERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003
CURRENT FILING DATE: 2003-11-26
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Meares, Claude
APPLICANT: Corneillie, Todh
TITLE OF INVENTION: Multi-Functional Antibodies
FILE REFERENCE: 023070-130910US
CURRENT APPLICATION NUMBER: US/10/625,047
CURRENT APPLICATION NUMBER: US/10/625,047
FRIOR PILING DATE: 2003-01-23
FRIOR FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                       STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218
                                                                                                                                                                             STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Publication No. US20040198962A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.9
Matches 209; Conservative
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US-10-723-003-42
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LENGTH: 218
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118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.7%; Score 755.5; DB 16; Best Local Similarity 70.5%; Pred. No. 5.2e-56; Matches 155; Conservative 16; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/995,693
FILING DATE: 29-No. US20020136721A1-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR FILING DATE: 2003-11-25
PRIOR PPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
ERQ ID NO 42
LENGTH: 235
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                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION:
TELEPHONE: 650/225-5416
TELEFAC. 650/225-981
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09995693
; Patent No. US20020136721A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
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68

Gaps

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Sequence 4, Application US/09848832

Sequence 4, Application US/09848832

Publication No. US20030165507A1

GENERAL INFORMATION:
APPLICANT: Hooper, Douglas
APPLICANT: Dietzschold, Bernhard

TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
FILE REFERENCE: HOOO1.NPO01.
FOR APPLICATION NUMBER: 05/09/848,832

CURRENT PILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/204,518

PRIOR APPLICATION NUMBER: 60/204,518

RUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO
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                                                                                                                                                                                                     DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
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                                                                                                                              SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS
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; Pred. No. 1.2e-55;
14; Mismatches 42;
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Pred. No. 1.7e-55;
                                                                                                                                                                                                                                                                                                                                       SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HOOPER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
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71.8%;
                                 66.3%;
71.8%;
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Matches 155; Conservative
                                                                       Conservative
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                                                     Similarity
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                                 Query Match
Best Local Simi
Matches 153;
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US-10-232-408-1
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                                                                                                                                                                                                                                                                                                                                                                                 128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187
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                                                                                                                                                    Gaps
                                                                                                                                                     4
                                                                                                                Length 220;
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Publication No. US20030118587A1
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compartible
COMPUTER: IBM PC compartible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,408
FILING DATE: 03-Sep-2002
CLASSIFICATION: CURKNOWN>
                                                                                                                                                     42;
                                                                                                              Query Match 66.3%; Score 751; DB 9; Best Local Similarity 71.8%; Pred. No. 1.2e-55; Matches 153; Conservative 14; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                          186 SKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-011-2001
APPLICATION NUMBER: US/08/952,235
FILING DATE: «UNALOWN-
PILING DATE: «UNALOWN-
APPLICATION NUMBER: 08/460368
FILING DATE: 02-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE DESCRIPTION: SEQ ID NO: 1:
                   TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Marschang, Diane L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 220 amino acids
TYPE: Amino Acid
     LENGTH: 220 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
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US-10-232-408-1
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Publication No. US20040013672A1

GENERAL INFORMATION:

APPLICANT: Dietzechold, Bernhard

APPLICANT: Dietzechold, Bernhard

APPLICANT: Dietzechold, Bernhard

APPLICANT: Dietzechold, Bernhard

APPLICANT: Hooper, Douglas C.

TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS

TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND USING THE SAME

TITLE OF INVENTION: NUMBER: US/10/461,148

CURRENT FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: US 60/314,023

PRIOR PILING DATE: 2001-08-21

PRIOR PILING DATE: 2001-06-21

PRIOR PILING DATE: 2001-05-04

PRIOR PILING DATE: 2001-05-04

PRIOR PILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PERSENCE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions; TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 69/848,832
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-16
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTESEQ for Windows Version 4.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 234;
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71.8%; Pred. No. 1.7e-55;
tive 13; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Best Local Similarity 71.89
Matches 155; Conservative
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Best Local Similarity 71.8<sup>†</sup>
Matches 155; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Human
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US-10-461-148-2
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4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP

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182
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80 ARFSGSGGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF
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Publication No. US20040120949A1
Publication No. US20040120949A1
GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Baumann, Michael
APPLICANT: Heider, Karl-Heinz
ITILE OF INVENTION: Compositions and methods for treating cancer using
TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
CURRENT APPLICATION NUMBER: US/10/704,522
CURRENT FILING DATE: 2003-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description of Artificial Sequence: Humanised; OTHER INFORMATION: Murine Antibody BIWA 8 Light Chain SEQ ID NO: US-10-150-475A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Adolf, G. et al.

TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REFERENCE: 1/1211
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/307,451
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                    183 LTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                            LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/10150475A; Publication No. US20030103985A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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ARPSGSLIGDKAALTITGAQTEDBARYFCALWYFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                 3 VITOSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP
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                                            123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Description of Artificial Sequence: Humanised; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: US-10-150-475A-4
                                                                                                                                                                                                                                                Length 213;
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                                                                                                                        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                            Query Match 66.0%; Score 747; DB 14; Best Local Similarity 72.2%; Pred. No. 2.4e-55; Matches 156; Conservative 13; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10704522;
Sequence 4, Application US/10704522;
Publication No. US20040120949A1
GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and methods for TITLE OF INVENTION: Cytotoxic CD44 Antibody Imm: FILE REFERENCE: 1/1414
CURRENT APPLICATION NUMBER: US/10/704,522;
CURRENT APPLICATION NUMBER: US 60/429,516;
PRIOR APPLICATION NUMBER: B 02024881
PRIOR PILING DATE: 2002-11-27;
PRIOR APPLICATION NUMBER: EP 02024881;
PRIOR FILING DATE: 2002-11-08;
NUMBER OF SEQ ID NOS: 9
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US-10-150-475A-4
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APPLICANT: Baum, Ankel
APPLICANT: Baum, Ankel
APPLICANT: Baum, Ankel
APPLICANT: Baum, Ankel
TITLE CANTEL Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cyctoxic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Chemotherapeutic Agents
FILE REFERENCE: 1/1383
CURRENT FILING DATE: 203-08-21
PRIOR PILING DATE: August 21, 2002
PRIOR PILING DATE: August 25, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                              OTHER INFORMATION: Humanised Murine Antibody BIWA 8 Light Chain
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                                                                                                                                                                                                                                                                                   Query Match 66.2%; Score 749; DB 16; Length 213; Best Local Similarity 72.2%; Pred. No. 1.7e-55; Matches 156; Conservative 14; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/429,516
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP 02024881
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10645215 Publication No. US20040126379A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                       ORGANISM: Artificial Sequence
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SEQ ID NO 8
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Search completed: June
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; Sublication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
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; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; FILE REFERENCE: 1/1383
; CURRENT FILING DATE: August 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
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                                                                                                               ; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain US-10-704-522-4
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66.0%; Score 747; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.4e-55;
Matches 156; Conservative 13; Mismatches 41; Indels
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SOFTWARE: Patentin Ver. 2.1
               SEQ ID NO 4
LENGTH: 213
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                                                                                                                                                                                                                                                APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/254,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-15-05
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PATENT NUMBER: US 10/006,593
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PATENT NOS: 134
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                             178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.5%; Score 742; DB 15; Best Local Similarity 70.8%; Pred. No. 6.6e-55; Matches 153; Conservative 16; Mismatches 43;
183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: antibody light chain US-10-307-724-122
                                                                                                                                                                          ; Sequence 122, Application US/10307724; Publication No. US20030232972A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: artificial sequence
                                                                                                                                                          US-10-307-724-122
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7, 2005, 16:18:38

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

June Run on:

7, 2005, 15:39:10 ; Search time 25 Seconds (without alignments) 839.010 Million cell updates/sec

US-09-671-953B-5 1132 1 RSAVVTQESALTTSPGETVT......BVTHQGLSXPVTKSFNRGEC 218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ig lambda chain v Ig lambda chain v Ig lambda chain v Ig kappa chain - m Ig lambda chain v Ig lambda - chain v Ig lambda-1 chain v Ig lambda chain v r Ig lambda chain v
\$06822 B54256 \$42772 \$16112 L2MS35 PC4203	PH1089 S14582 S06821 S52028 PH1090 A56169 S14584 PH1088
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114 217 219 219 235	99 99 113 219 97 116 210 99
8 C C C C C C C C C C C C C C C C C C C	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	484.5 4882 4882 482 477 477 475.5 472
011264866	C B B B B B B B B B B B B B B B B B B B

## ALIGNMENTS

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Ig kappa chain NIG26 precursor - human C; Species: Homo sapiens (man) C; Species: Schacession: J80242 R; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, A; Description: Structure relationship of kappatype light chains with AL amyloidosis: Mu A; Reference number: J80241
```

A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 ALI:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match
65.4%; Score 740; DB 2; Length 215;
Best Local Similarity 70.4%; Pred. No. 7.9e-49;
Matches 152; Conservative 17; Mismatches 43; Indels

ų; 4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62 Gaps 4 ð

63 ARFSGSLIGDKAALTIITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122 g ઠે

PPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182 셤 П 8

183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218 ò 셤

180

RESULT 2

JE0244

JE0244

JE0244

JEG Kappa chain NIG2 precursor - human

C; Species: Homo sapiens (man)

C; Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

R; Alia, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

B; Alia, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

A; Reference number: J50244

A; Reference number: J50243

A; Resedues: 1-215 ALIS

C; Superfamily: immunoglobulin V region; immunoglobulin homology

F; 16-90/Domain: immunoglobulin homology < INM>

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Query Match
Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                Ig lambda chain V region MabB23 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: PC4156
R; Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Cene 169, 237-239, 1996
A; Title: Cloning and characterization of CDNAs coding for heavy and light chains of A; Reference number: PC4155
A; Rocession: PC4156
A; Molecule type: mRNA
A; Residues: 1-214 < kWA>
A; Residues: 1-214 < kWA>
A; Residues: GB: U28667; NID: 91262178; PIDN: AAC52488.1; PID: 91262179
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 1-214/Product: light chain #status predicted < kMAT>
F; 98-110/Region: V region
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                                                                                                                                                           2 AVVIQESALITSPGETVILICRSNIGAVITSNYASWVQEKPDHLFTGLIGGINNRVPGVP
                                                                                                     VLTÓSPATLSVSPGERATLSCRAS--QSVHSNLA-WYQQKPGQAPRLLIYRASTRATGIP
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                                                                      VVTQESA-LTTSPGETVTLTCRSSICAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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 Length 215
                                     39; Indels
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Query Match 64.4%; Score 729; DB 2; Best Local Similarity 71.2%; Pred. No. 5.4e-48; Matches 156; Conservative 14; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.0%; Score 724.5; DB 2
66.5%; Pred. No. 1.2e-47;
iive 23; Mismatches 43
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Tall (KAU cold agglutinin) - human Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cispecies: Alone-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000 Ciscossion: A23746 Billoni, J.; Ghiso, J.; Goni, F.; Frangione, B. A. Blol. Chem. 266, 28842 1991 Airle Airle Chem. 266, 28842 1991 Airle Chem. 267, 2885-28842 Airle Chem. 268, 28842 Airle Chem. 268, 28842 Airle Chem. 268, 28842 Airle Chem. 268, 28842 Airle Chem. 2884 Structure of the Fab fragment of protein KAU, a monoclonal immunogla Airle France number: A23746; MUID:91131575; PMID:1993660
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                                                     immunoglobulin homology
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                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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                                                                                                                                      63.3%; Score 716; DB 2;
69.7%; Pred. No. 5.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.3%; Score 682.5; DB 2
Best Local Similarity 66.8%; Pred. No. 1.7e-44;
Matches 145; Conservative 14; Mismatches 53
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                                                                                                                                                                                        13; Mismatches
A;Molecule type:.protein
A;Residues: 1-215 <ALI>
Csuperfamily: immunoglobulin V region;
F;16-90/Domain: immunoglobulin homology
                                                                                                                                                                                        Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: JE0241
A;Accession: JE0241
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A; Molecule type: DNA
A; Residues: 1-106 <HIE>
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Matches 117; Conserv
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C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Date: 28-Reb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
C;Accession: S06084
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNA
A;Reference number: S06084; MUID:90016888; PMID:2508067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
R;Parances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S. EMBO J. 13, 5937-5943, 1994
A;Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S. EMBO J. 13, 5937-5943, 1994
A;Reference number: S52059; MUID:95112804; PMID:7813432
A;Status: preliminary
A;Residues: Preliminary
A;Residues: 1-135 < FRA>
C;Superfamily: pre-B cell omega light chain; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                           63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                 Length 215;
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 < LEGO-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology < IMM>
                                                                                                                                                               Query Match 59.6%; Score 675; DB 2; Length 21 Best Local Similarity 68.8%; Pred. No. 6.3e-44; Matches 148; Conservative 15; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain precursor - rat
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Matches 113; Conservative
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Is kappa chain C region - human

(Species: Homo sapiens (man)

(Species: Homo sapiens (man)

(Species: Homo sapiens (man)

(Species: Homo sapiens (man)

(Spaces: Jan-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004

(Spaces: Jan-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004

(Spaces: Jan-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004

(Spaces: Jan-Dec-1980 #sequence_revision B.A.; Rutishauser, U.; Edelman, G.M.

Ricottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.

A; Fitle: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequence A; Molecule type: protein

A; Accession: B90562

A; Molecule type: protein

Biochemistry 9, 3188-3196, 1970

A; Title: The covalent structure of a human gammaG-immunoglobulin. X: Intrachain disulfine

A; Molecule type: protein; Bu, disulfide bonds

B; Suter, L.; Barnikol, H.U; Watanabe, S.; Hilschmann, N.

A; Title: Die primaerstruktur einer monoklonale Immunglobulin-L-Kette vom kappa-Typ, Su, A; Contents: Bance Jones protein Ti

A; Accession: A94651

A; Accession: A94651

A; Accession: A94651
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A;Molecule type: protein
A;Residues: 1-106 <SUT>
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
R;Hieter, P.A.; 199-207, 1980
A;Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conser
A;Reference number: A90806; MUID:81042304; PMID:6775818
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A,Note: the sequence was determined from the germline gene
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, In Gamma Globulins: Structure and Function, Franck, F.; and Shugar, D., eds., pp.57-74, A;Reference number: A94417
A;Contents: Bence Jones protein Roy
A;Accession: A94417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 SIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSM 201
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A;Molecule type: mRNA
A;Residues: 1-240 <CRO>
A;Residues: 1-240 <CRO>
A;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1.20/Domain: signal sequence #status predicted <SIG>
F;21.240/Product: IG kappa chain #status predicted <MAT>
F;21.222/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                              48.8%; Score 552.5; DB 2
llarity 53.4%; Pred. No. 1.2e-34;
Conservative 24; Mismatches 73
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Query Match
Best Local Similarity 96.3%;
Matches 104; Conservative
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                Biochem. 122, 322-329, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: $52450
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No Molecule 1744, 72.065.56.70, 58-82, 12, 84-106, 4HID.

No Molecule 1744, 72.065.56.70, 58-82, 12, 84-106, 4HID.

Rivitor this sequence has the Inv (1.2) allotypic marker, 45-Ala and 83-Leu
Rivitor this sequence has the Inv (1.2) allotypic marker, 45-Ala and 83-Leu
Rivitor this sequence has the Inv (1.2) allotypic marker, 45-Ala and 83-Leu
Rivitor this sequence maker, 840-859.

Argetescence number: A91639.

Argetescence number: A91649.

Argetescence number: A91639.

Argetescence number: A91649.

Argetescence number: Argetescence number: Argetescence number: Argetescence number: Argetescence number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Matches 105;
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A,Title: Construction, bacterial expression, and characterization of hapten-specific sin A,Reference number: PC4402
A,Accession: PC4402
A,Accession: PC4402
A,Molecule type: DNA
A,Residues: 1-287 <802>
C,Keywords: fusion protein
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A1790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
A;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.Se A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an A;Reference number: A92686; MUID:89034213; PMID:3182835
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C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
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submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of
A;Reference number: S52445
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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Pred. No. 9.1e-34;
0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

48.0%; Score 543.5; DB 4
Best Local Similarity 53.4%; Pred. No. 6.9e-34;
Matches 126; Conservative 14; Mismatches 49
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ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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Best Local Similarity 50.5
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 94.4
Matches 102; Conservative
                                                                                           A; Contents: H2020
A; Accession: A90780
                                                                                                                                                                                                                                                                                                                                                   A; Accession: C93282
                                                                                                                                                                                                                                                                                                                                A; Contents: S43
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C;Species: Mus musculus (house mouse)
C;Date: 24-Sep-1981 #sequence revision 24-Sep-1981 #text change 09-Jul-2004
C;Date: 24-Sep-1981 #sequence revision 24-Sep-1981 #text change 09-Jul-2004
C;Accession: B93815; B93775; C93775; A93784; B93784; C93784; A90780; C93282; A01995
R;Burstein, Y; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               show no differences from MOPC 104E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:P01724
A;Note: this precursor was synthesized in a cell-free system directed by messenger RNA
d after synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43)
                     A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Residues: 1-220 <SCH>
A;Cross-references: GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPLTFGGGTKLE-LKRADAAPTV 121
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                                                                                                                                                                                                                                                                                                                                                        3 VMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTRES
                                                                                                                                                                                                                                                                                                     4 VVTQE-SALTTSPGETVTLTCRSS---IGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAP
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                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains. A;Reference number: A93775; WUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
                                                                                                                                                                                                                                                       5,
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                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda-chain sequences.
A;Feterence number: A93784; MUID:73229669; PMID:4516208
A;Contents: J558; S104; S178
                                                                                                                                                                                                 Query Match 46.9%; Score 530.5; DB 2; Best Local Similarity 51.6%; Pred. No. 5e-33; Matches 113; Conservative 26; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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A,Residues: 20-129 <AP2>
A,Note: compositions and partial sequences of RPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 'Z', 21-25,'Q','27-129 <APP>
A,Accession: C93775
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A, Molecule type: protein
A, Residues: 1-29 <BUR>
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A, Residues: 20-129 <CES>
A, Accession: B93784
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A; Accession: A31790
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C;Complex: http://www.district.com/publin.neterotetramer subunit consists of two identical light (kage hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l. C;Superfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer: pyroglutamic acid F;1-19/Domain: signal sequence #status experimental <SIG>F;20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>F;20-129/Domain: immunoglobulin homology <IMM>F;20-120/Domain: immunoglobulin homology <IMM>F;20-120/Domain: immunoglobulin homology <IMM>F;20-120/Domain: immunoglobulin homology <IMM>F;20-120/Domain: immunoglobulin phomology <IMM>F;20-120/Domain: immunoglobulin homology <IMM>F;20-120/Domain: immunoglobulin homology <IMM>F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental chain predicted
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A; Residues: 1.43, T. 45-50, G, 52-58, E, 60-89, D, 91-129 <BER>
A; Residues: 1.43, T. 45-50, G, 52-58, E, 60-89, D', 91-129 <BER>
A; Note: the sequence was determined from the differentiated gene
R; Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore,
Nature 298, 380-382, 1982
A; Title: Sometic variants of murine immunoglobulin lambda light chains.
A; Reference number: A93282; MUID:82220143; PMID:6283385
R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic
A;Reference number: A90780; MUID:79084170; PMID:103630
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A;Molecule type: mRNA
A;Residues: 1-235 <FIS.
A;Cross-references: EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID:954829
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-111/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-58, E',60-89,'D',91-98,'T',100-105,'M',107-129 <BOJ
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.
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50.5%; Pred. No. 2.3e-32;
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Pred. No. 3.7e-33;
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123 PPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182

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RESULT 15
S06819
Ig lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: S06819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Titler iII, A.; Glasel, MuD:90064531; PMID:255519
A;Accession: S06819
A;Accession: S06819
A;Accession: S06819
A;Accession: S06819
A;Accession: S06819
C;Accession: S06819
A;Cross-references: EMBL:X17168; NID:952251; PIDN:CAA35046.1; PID:9930172
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology 
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62
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46.0%; Score 521; DB 2; Length 113
Best Local Similarity 94.4%; Pred. No. 1.3e-32;
Matches 102; Conservative 1; Mismatches 5; Indels
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Search completed: June 7, 2005, 16:01:07 Job time : 26 secs

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06pim29
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum Match 1008
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Maximum DB seq length: 2000000000
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43	42	40	39	38	38	38	38	38	37	37	37.8	37	37	
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=1.10. Med=1.10. Med
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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ALIGNMENTS
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-21.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_W.
InterPro; IPR003596; Ig_W.
InterPro; IPR004596; Ig_V.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
PR051TE; PS00396; IG_LIKE; 2.
PR051TE; PS00290; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                      Created)
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Submitted (OCT-2001) to the
EMBL; BC016380; AAH16380.1;
HSSP; P01837; IKCU.
                                                                                                                                                                                                                                        PRELIMINARY;
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Catarrhini, Hominidae, Homo.
                                                                                            4,
                                                       Length 235;
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Submitted (UN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037392; AAH73792.1; -.
InterPro; IPR0013599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR0013597; Ig-c1.
InterPro; IPR001597; Ig-c1.
InterPro; IPR001596; Ig-MHC.
InterPro; IPR001596; Ig-WHC.
Pfam; PPF0564; C1-set; 1.
Hypothetical protein.
SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                          LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
                                                   64.8%; Score 734; DB 2; 70.4%; Pred. No. 1.5e-56;
                                                                                                                                                                                                                                                                                                                                                    LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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                                                                       Best Local Similarity 70.4%; Pred. No. 1.5e
Matches 152; Conservative 18; Mismatches
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Mammalia; Eutheria; Primates;
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                                                     Query Match
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                     Length 235;
                                                                                                                                                                                         41; Indels
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Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073791; AAH73791.1; -.
INCEPPC; IPR003599; IG.
InterPro; IPR007110; IG-like.
SMART; SM00409; IG; 2.
SMART; SM00401; IGc1; 1.
PROSITE; PS00436; IGv; 1.
PROSITE; PS00239; IG_LIKE; 2.
PROSITE; PS00239; IG_MHC; UNKNOWN_1.
SEQUENCE 235 AA; 25765 WW; 4360C36B6D4133F5 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                 Query Match
64.8%; Score 733; DB 2;
Best Local Similarity 70.5%; Pred. No. 1.9e-56;
Matches 153; Conservative 17; Mismatches 41;
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Homo sapiens
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A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,
A Basa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Basa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Basa S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Trepannski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Gores F.J., Marra M.A.,
A Gores F.J., Marra 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels
                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 236 AA; 25751 MW; SBFE6A087AFAC437 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                       64.7%; Score 732; DB 2; 70.0%; Pred. No. 2.3e-56;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003056; Ig_WHC.
Pfam; PF00404; Ig_V.
Pfam; PF00404; Ig_2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
PR05ITE; PS0085; IG LIKE; 2.
PROSITE; PS00836; IG_LIKE; 2.
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TISSUE=Skeletal Muscle;
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TISSUE=Skeletal Muscle;
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Q7Z3Y4
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RADILINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RADILINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA STRAUSELY R.L., Feligold B.A., Grouse L.H., Derge J.G.,
RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
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RA Richards S., Morley K.C., Scherchenko S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rhakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rhying M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
RT And mouse cDNA sequences.";
R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 236;
                       to the EMBL/GenBank/DDBJ databases
                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_W.
SWART; SM00406; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein:
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.3%; Score 727.5; DB 2 70.7%; Pred. No. 5.7e-56; ive 15; Mismatches 43
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Strausberg R.;
Submitted (MRR-2001) to the
EMBL; BC05332, AAH05332.1;
HSSP; P01834; 1HEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 152; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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rissue-Lung;
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MEDINES-2288257; PubWed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haieh F.,
A stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Richards S. W., Touchman J.W., Green E.D., Dickson M.C.,
A Rakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                       Straubberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
REMBL, BC066256; AAH56256.1;
RINGEPRO; IPR001310; Ig-11ke.
RINGEPRO; IPR001350; Ig-C1.
RINGEPRO; IPR0013066; Ig-WHC.
RINGEPRO; IPR0013066; Ig-WHC.
R PROSTIE; PS00835; IG-LIKE; 2.
R PROSTIE; PS00835; IG-LIKE; 2.
R PROSTIE; PS00290; IG-MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 234;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.2%; Score 727; DB 2;
68.2%; Pred. No. 6.3e-56;
iive 20; Mismatches 44;
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Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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RA SQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA STRANBEPET R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA STRANBEPET R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA HISCHUI S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOPKINS R.F., JORDAN H., Moore T., Wang J., Hableh F.,

RA HOPKINS R.F., JORDAN H., Moore T., Wax S.I., Wang J., Hableh F.,

RA Brownstein M.J., Usdin T.B., Torshiyki S., Carninci P., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Torshiyki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S.W. Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 LTQSPSFLSASVGDRVTITCRASQG---ISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 RFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSSPPTFGGGTKVEI-KRTVAAPSVFIFP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                          Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034141; AAH34141.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 236 AA; 25603 WW, 8BC561106861213F CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Eukaryota. March
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
63.9%; Score 723.5; DB 2
Best Local Similarity 70.7%; Pred. No. 1.3e-55;
Matches 152; Conservative 14; Mismatches 44
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                                                                                                                                                                                                                                                                   InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR00310; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
PEam; PP07654; Cl-set; I.
SMART; SM004007; IGC1; I.
SMART; SM004007; IGC1; I.
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                                                                                                                                                                                                                                                 HSSP; P01607; 1AR2
                                                                     SEQUENCE FROM N.A
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Local Similarity
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MEDLINE-22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
Straubsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moorer T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Grandlis of more than 15,000 full-length human "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VIQE-SALTISPGETVILICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Butterfield Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 236;
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                                                                                                                                                 Strausberg R.;
Strausberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073/63; AAH73763.1; -.
InterPro; IPR0013599; Ig.
InterPro; IPR001310; Ig-like.
InterPro; IPR0013597; Ig.cl.
InterPro; IPR0013597; Ig.cl.
InterPro; IPR0013596; Ig_WHC.
Pfam; PP07654; Cl-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEGUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gepsse;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.8%; Score 722.5; DB 2;
69.3%; Pred. No. 1.6e-55;
ive 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                 FRANT; SMO0409; IG; 2.
SMART; SMO0407; IG; 1.
SMART; SMO0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149; Conservative
                                                                       вефпепсев.
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                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
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Best Local Similarity
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                                                                       CDNA
                                                                       and mouse
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Hellron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ARFSGSLIGDKAALTITGAQTEDEARYFCALW-YSCLWVFGGGTKLTVLSRTVAAPSVPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 VLTQSPGTLSFSPGERATLSCRAS--QTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VVTQE-SALITISPGETVTLICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVP
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TISSUE-Spleen;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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A INTERPRO; IPR003599; IG.

A INTERPRO; IPR003599; IG.

A INTERPRO; IPR003006; Ig_MHC.

A INTERPRO; IPR003006; Ig_MHC.

A INTERPRO; IPR003006; Ig_WHC.

A SMART; SM00409; IG; 2.

A SMART; SM00406; IGV; 1.

A SMART; SM00406; IGV; 1.

A PROSITE; PS50835; IG_LIKE; 2.

A PROSITE; PS50835; IG_MHC; UNKNOWN_1.

A HYPOCHECICAL DYCCEIN.

A HYPOCHECICAL DYCCEIN.

A SEQUENCE 236 AA; 25773 MW; 953B37BEB4FF5F27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Glandular pool- thyroid;
StraubBorg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062704; AAH62704.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
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                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusha R., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., TOSHIYWKI S., Carninci P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McZham P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
A Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
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    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Sofbetz T.E., Brahalon M., Soares M.B., Bonaldo M.F., Casavant T.L., Sofbetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Muzny D.W., Sodergren B.A., Gunzatare P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Muzny D.W., Sodergren B.M., Rodrigues S., Sanchez A., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC073793; AAH73793.1; ...
R InterPro; IPR00310; Ig-like.
R InterPro; IPR00310; Ig-like.
R InterPro; IPR00310; Ig-like.
R InterPro; IPR00310; Ig-like.
R InterPro; IPR003106; Ig-MHC.
R InterPro; IPR003106; Ig-MHC.
R Edm; PP00047; Ig-set; I.
R SMART; SM00407; IG, 2.
R SMART; SM00406; IG, 2.
R SMART; SM00406; IG, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AA; 25646 MW; DF32B580BAD19E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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69.4%; Pred. No. 2.1e-55;
iive 15; Mismatches 47
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
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Matches 150, Conservative
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SEQUENCE 23
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PROSITE; PS50835; IG LIKE; 2. PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

and mouse

SEQUENCE FROM N.A. rissum=Spleen;

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141
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                                                                                                                                                   64 RFSGSLIGDKAALTIITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP
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                                                                                                                              5 VTQE-SALTISPGETVTLICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVPA
                                                                                          Gaps
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21
                                                     DB 2; Length 236;
Hypothetical protein.
SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein.
Homo sapiens (Human).
                                                   Query Match 63.6%; Score 720.5; DB 2; Best Local Similarity 69.3%; Pred. No. 2.4e-55; Matches 149; Conservative 17; Mismatches 44;
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1D Q6
AC Q6
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DT 05
DT 05
OS H0
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OS-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hymo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

SEQUENCE FROM N.A. TISSUE=Spleen;

NCBI\_TaxID=9606;

236 AA

PRELIMINARY;

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                                                                  Astraubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul E.S., Zeeberg B. S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.P., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tonshiyuki S., Carninci P., Frange C.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Myliting M., Madan A., Young A.C., Shangues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                   IISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003306; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; Cl.set; I.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
Hypothetical protein.
SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;
 Eutheria; Primates; Catarrhini; Hominidae; Homo
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.4%; Score 717.5; DB 2 69.6%; Pred. No. 4.4e-55;
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                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
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P01837; 1KCU.
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Brain;
                                    SEQUENCE FROM N.A.
               NCBI_TaxID=9606;
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Best Local Simi
Matches 151;
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RC TISSUE-Primary B-Cells;

RA MILINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altasaner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,

RA Altaschul S.F., Zeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Plakesley R.W., Touchman M., Madan A., Rodriques S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.J., Dickson M.C.,

RA Rabesley R.W., Touchman J.W., Schentz J., Myers R.M., Butterfield Y.S.,

RA KILMAN M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

Tand mouse CDNA sequences.,

Tand mouse CDNA sequences.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTQE-SALTISPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 MTQSPSSVSASVGDRVTITCRASQG---ISSWLAWYQQKPGKAPKILIYAASSLQSGVPS
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                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073764, AAH73764.1; -.
InterPro; IPR003599; Ig. 11ke.
InterPro; IPR007101 Ig-11ke.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003597; Ig. v.
InterPro; IPR003597; Ig. v.
InterPro; IPR00369; Ig. v.
InterPro; IPR00369; Ig. v.
InterPro; IPR00369; Ig. v.
InterPro; IPR00309; Ig. v.
InterPro; IPR00309; Ig. v.
InterPro; IRV0409; IG.; I.
INTERPRO; IGC1; I.
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SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.2%; Score 715.5; DB 2
Best Local Similarity 69.3%; Pred. No. 6.6e-55;
Matches 149; Conservative 19; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                    [1] -
SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=9606;
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236 AA

05-JUL-2004 (TrEMBLrel. 27, Created)

PRELIMINARY;

Q6GMX8

RESULT 12 Q6GMX8 us-09-671-953b-5.rup

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Q6РІН4
Q6РІН4;
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MEDINE-2288257; PubMed=12477912; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heieh F.,
A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 RCAIQLTQSPSSLSASVGERVTITCRASQG---ISSALAWYQQKPGKPPKLLIYDASTME 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 69.1%; Pred. No. 6.8e-54;
Matches 152; Conservative 15; Mismatches 47; Indels
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO29444; AAH29444.1; -.
HSSP; P01607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS02299; IG_MHC; UNKNOWN_1.
Hypotherical protein.
SEQUENCE 236 AA; 25741 MW; BDS0AF071FEEE351 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                        Last sequence update)
Last annotation update)
                                                   236 AA
                                                                                                   Created)
                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR0013599; Ig.
Interpro: IPR007110; Ig-11ke.
Interpro: IPR003597; Ig.c1.
Interpro: IPR003506; Ig.MC.
Interpro: IPR003596; Ig.WC.
Interpro: IPR003596; Ig.W.
Pfam; PP07654; Cl-set; I.
SMART; SM00409; IG; I.
SMART; SM00407; IGc1; I.
                                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                PRELIMINARY;
                                                                                                                                                                   Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
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RESULT 13
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TISSUE=Lung;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altachar R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soates M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loguellann N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RIChards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

RA Goresation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VTQE-SALTISPGETVTLICRSSIGAVTISNYANWVQEKPDHLFTGLIGGINNRAPGVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO34146; AAH34146.1; -.
HSSP; PO1607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 236 AA; 25871 MW; BE01A28CD06EEE26 CRC64;
218
                             197 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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                                                                                                                                                                                                                      236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
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SWART; SW00407; IGC1; I.
SWART; SW004009; IG; I.
PROSITE; PS00835; IG_LIKE; I.
PROSITE; PS00835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                  (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 148; Conservative
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                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissum=Lung;
                                                                                                                                                                                                                                                                                  05-JUL-2004
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RA Alasoner R.D., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Alaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Alaschul S.F., Jordan H., Moore T., Wax S.I., Wang J., Heish F.,
A pottins R.E., Jordan H., Moore T., Wax S.I., Wang J., Heish F.,
A backnastein M., Soares M.B., Bonaldo M.F., Casnant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Rahay J., Helton E., Ketteman M.J., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rhaby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
The mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                  142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
61.6%; Score 697; DB 2; Length 239;
Best Local Similarity 67.4%; Pred. No. 2.8e-53;
Matches 149; Conservative 15; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
SEQUENCE FROM N.A.
TISSUE=Lung;
Strausbeeg R.;
Submitted (FB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAH22362.1; -.
PIR; S22668; S22658.
PIR; S4095; S34095.
PIR; S40374; S40374.
PIR; S42267; S42268.
PIR; S42268; S42268.
PIR; S42268; S42268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 protein.
239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                    184 TLSKADYBKHKVYACEVTHQGLSXPVTKSFNRGEC 218
202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
                                                                                                                                                                                             239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
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Interpro; IPR003597; Ig_cl.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF07654; Cl-8et; l.
SMART; SM00406; IGv; l.
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE 23
                                                                                                                                                        RESULT 15
Q8TCD0
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Search completed: June 7, 2005, 16:00:11 Job time: 113 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 7, 2005, 15:28:46; Search time 114.5 Seconds (without alignments) 736.365 Million cell updates/sec Run on:

US-09-671-953B-7 1134 1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched: 2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2001s:\*

5: geneseqp2001s:\*

6: geneseqp2003s:\*

7: geneseqp2003bs:\*

8: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	rosof.		-	-	-	_	Adq98051 Chimeric				Ad192471 Antibody		•				_		-	_	_	Aaw07528 Anti-HGF			Light	Abu08018 Human mon	Adf65776 Human mon
SUMMARIES	f	1D	AAB20360	AAB20359	AAB20358	ADQ98050	ADQ98051	ADR23362	AAE27925	ABB82834	ADL92471	AAW82740	AAB08025	AAE34878	ADL15445	AD000853	AAE35326	AAE34877	ADL15441	ADO00849	ADP79579	AAW07528	ADQ31891	ADQ31885	AA014066	ABU08018	ADF65776
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	1	rengra	218	218	218	218	218	215	235	235	213	235	235	213	213	213	213	213	213	213	236	220	215	215	234	234	234
	Query	March	99.8	98.9	98.1	95.5	95.4	68.7	67.0	67.0	6.99	8.99	66.5	66.4	66.4	66.4	66.2	66.2	66.2	66.2	66.2	66.1	65.8	9.59	65.6	9.59	9.59
	į	Score	1132	1122	1113	1083	1082	779	759.5	759.5	759	757	754.5	753	753	753	751	751	751	751	751	750	746	744	743.5	743.5	743.5
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	•	Aay93731 The kappa	Aae35886 Human 4.8	_	Abj38595 Hepatitis	Aaw05830 Humanised	_	Abp55483 CJRA05 pr	_	Aae33521 Human AQC	Adp79583 2H7.v16 L	Aaw06180 Humanised	Aay34096 Partial a	_	Aar12128 1B1 IgG a	Aar13111 1B1 IgG a	Aar13018 1B1 IgG a	Aab83157 Gangliosi	Abr01469 Human ant
ADJ92516	AAY93704	AAY93731	AAE35886	ADK70470	ABJ38595	AAW05830	AAY92239	ABP55483	ADQ16702	AAE33521	ADP79583	AAW06180	AAY34096	ADH34591	AAR12128	AAR13111	AAR13018	AAB83157	ABR01469
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234	233	233	233	239	240	213	234	234	215	213	232	235	236	214	349	414	414	213	215
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65.	65.	65.	65.	65	65.4	65	65.	65.	65.	65	65	64.9	64.	64	64	64	64	64	64
743.5	743	743	743	743	741.5	741	740.5	739.5	739	738	738	736	736	735.5	735.5	735.5	735.5	735	735
56	27	28	58	30	31	33	8	34	35	36	37	88	30	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

AAB2	AAB20360 standard. nrotein.	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
ξ×	AADZV300 Standard, F	
AC	AAB20360;	
X		
占:	11-JUN-2001 (first entry)	entry)
¥ E	Anti-chelate antibod	antibody CHA255 light chain mutant 895C.
×		
X	Antibody engineering;	y, metal chelate; CHA255; indium; EDTA; tumour;
K	cancer; therapy; mut	therapy; mutant; mutein.
Ž	•	
SO	Mus musculus.	
SO	Synthetic.	
ž		
Æ	•	Location/Qualitiers
FT	Region 1.	
FT	/1at	
FT	`	
FT	Region 24.	.37
FŢ	•	,
FŢ	/not	/note= "complementarity determining region 1"
FT	Region 38.	.52
FT	`	els
FT	/not	/note= "framework region 2"
FT	Region 53.	5359
F		
FT	lou/	/note= "complementarity determining region 2"
ΡŢ	Region 60.	. 92
T.		
FT	ou/	/note= "framework region 3"
FT	Region 93.	1.0
FT	`	el=
FT	ou/	note= "complementarity determining region 3"
FT	Misc-difference 95	
FT	_	note= "replaces Ser of wild-type sequence"
FT	Misc-difference 100	
FT	ou/	note= "encoded by GTR"
FT	Region 101.	131
FT	`	
FT	ou/	note= "framework region 4"
FT	Misc-difference 112	
FT	_	note= "encoded by CGW"
FT	Misc-difference 113	
FT	_	note= "encoded by ACK"
F.	Misc-difference 206	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
H	ou/	note= "encoded by Adı"

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Key
Region
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RESULT 2
                      AAB20359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The cactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain variable covalent bond. The present sequence is that of the light chain variable region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C mutation. As an example of the method of the invention, rational computer added design was used to develop an indium-EDTA chelate to covalently bind to CHA255 bund to a tumour and then to covalently attach the covalently to CHA255 bund to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a human/mouse chimeric Fab fragment that could be expressed in Escherichia coli, and the synthesis and screening of benzyl-EDTA chelates carrying viac, in this Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site catered antibody to which the chelate bound. This was accomplished by site anti-chelate antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPARFSGSLIGDKAALTITGAQTEDBARYFCALWYCNLWVFGGGTKITVLSRTVAAPSVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                  /note= "encoded by TYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 14; 100pp; English
                                                                                                                                 27-SEP-2000; 2000WO-US026619
                                                                                                                                                                        99US-0156194P
                                                                                                                                                                                        31-MAY-2000; 2000US-0208684P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity luv.
Matches 218; Conservative
                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                   Chmura A;
                                                                                                                                                                                                                                                                                                          WPI; 2001-244971/25.
N-PSDB; AAF30635.
Misc-difference 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 218 AA;
                                                      WO200122922-A2
                                                                                                                                                                        27-SEP-1999;
                                                                                                                                                                                                                                                                       Meares C,
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Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
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                                                                             engineering; metal chelate; CHA255; indium; BDTA; tumour;
                                                                                                                                                                                           "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                   'note= "complementarity determining region 3"
                                                                                                                                                                                                                                                        "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                 101. .131
/label= FR4
/note= "framework region 4"
                                                                                                                                                               "framework region 1"
                                                                                                                                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                          "framework region 2"
                                                           Anti-chelate antibody CHA255 light chain.
                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                            by ACK"
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                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                            /label= FR3
/note= "framework
AAB20359 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                          'note= "encoded
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31-MAY-2000; 2000US-0208684P.
                                                                                                                                                                                                                                                                                               93. .100
/label= CDR3
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|abel= FR1
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                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                         cancer; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200122922-A2.
                                                                                                            Mus musculus
                                       11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2001
                    AAB20359;
                                                                               Antibody
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metal chelate against which the wild-type antibody is raised. The metal chelate against which the wild-type antibody is raised. The cactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form covalent bond. The present sequence is that of the light chain of antibody chelate indium-EDTA monoclonal antibody CHA255. As an example of the method of the invention, rational computer-aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was indium-EDTA chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a human/mouse chimeric Fab fragment that could be expressed in Escherichia coli, and the synthesis and screening of benzyl-EDTA chelates carrying weakly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a cargeting moiety when desired. A reactive site was incorporated into the antibody by engineering a conjugate at location Asn-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site chiracted mitospering of a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1122; DB 4; Length 218; Pred. No. 2.3e-78; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody engineering; metal chelate; CHA255; indium; EDTA; cancer; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-chelate antibody CHA255 light chain mutant N96C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding the wild-type of the anti-chelate antibody
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Best Local Similarity 99.5%;
Matches 217; Conservative (
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/label= CDR1
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|abel= CDR2
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label= FR1
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/label= FR2
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/note= "complementarity determining region 2"

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The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The complementarity determining region (CDR) that selection proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain variable contained bond. The present sequence is that of the light chain variable corregion of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C caided design was used to develop an indium-EDTA chelate to covalently consolently to CHA255 bound to a tumour and then to covalently attach the covalently to CHA255 bound to a tumour and then to covalently attach the covalently to CHA255 bound to a tumour and then to covalently attach the covalently and the spitheds and screening of CHA255 to construct a involved cloning the variable domains of CHA255 to construct a consoler to the antibody, thereby trapping it at the tumour site. This coli, and the spitheds and screening of CHA255 to construct a coli, and the spitheds and screening of Denzyl-EDTA chelates carrying coli, and the spitheds and screening of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A vivo. This Fab can be conjugated into the antibody by singineering a Cys creative site was incorporated into the antibody by engineering a Cys creative site was incorporated into the hight chain, near the region of the antibody to which the chelate bound. This was accomplished by site consisted mutagenesis of a nucleic acid encoding the wild-type of the conjugated or ser-eps of the ser-eps or the region of the antibody to which the chelate bound and the coding the wild-type of the coding the series of the ser-eps of the ser-eps of the ser-eps of the ser-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
                                                          93. .100
/label= CDR3
/note= "complementarity determining region 3"
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                                                                                                                                       note= "replaces Asn of wild-type sequence"
50. .92
/label= FR3
/note= "framework region 3"
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                                                                                                                                                                                                                                                                                      note= "encoded by CGW"
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                                                                                                                                                                                                                                                                                                                                                                     "encoded by
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99.1%;
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31-MAY-2000; 2000US-0208684P.
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                                                                                                                                                                                                                         label= FR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-244971/25.
N-PSDB; AAF30633.
                                                                                                                                                                 Misc-difference 100
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Best Local Similarity
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                                                                                                                          Misc-difference
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Sequence 218 AA;
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Chimeric.
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                                                                                                   61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                       VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                                                                     IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vel mutant antibody comprising reactive site not present in wild-type antibody and antigen recognition domain that recognizes macrocyclic tal chelate having four nitrogen atoms, useful for treating cancer or
                                                          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                RSAVVTQESALTISPGETVTLICRSSIGAVITSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              murine; mouse; chimeric; human; TTCL; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography.
Gaps
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2; Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            ADQ98050 standard; protein; 218 AA
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22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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216; Conservative
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N-PSDB; ADQ98054.
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Chimeric.
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ADQ98050
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reactive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody comprises a targeting moiety that binds specifically to a cell via a cell surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex. Is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide sequence is the chimeric mutine antibody 2012.5 variable light chain protein fused to the human anti-tetanus toxin antibody kappa light chain constant region
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Pred. No. 2.3e-75;
0; Mismatches 9;
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22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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Best Local Similarity 95.9
Matches 209; Conservative
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chelating agents to multi-inncitonal anitoboates that recognized chelates. Specifically, it refers to an antibody that comprises a metal chelates. Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate chelate bound to an antigen recognition domain, where the metal chelate caretive functional group of complementary reactivity to the reactive functional group of complementary reactivity to the reactive functional group of complementary reactivity to the coverent bond between the reactive site of the antibody and the caretive functional group of the metal chelate. The present invention of reactive functional group of the metal chelate. The present invention comprises using these antibodies for in vivo imaging where the antibody complex. Surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide sequence is the chimeric mutant NSSC murine antibody 2D12.5 variable light chain
                                                                                                                                                                                                                                                                                              Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to multi-functional antibodies that recognise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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Pred. No. 2.7e-75;
0; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 41; SEQ ID NO 28; 208pp; English.
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ilarity 95.9%;
Conservative 0
(REGC ) UNIV CALIFORNIA
                                                                                   Corneillie
                                                                                                                                                                          2004-580725/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases.
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les 209; Conserv
                                                                                                                                                                                                                        N-PSDB; ADQ98055
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                                                                                                                                                                                                                                    IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                                                                                                                                                     VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF
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Sequence 215 AA;

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Human, CD72, B-lymphocyte; receptor; scFv; antibody; cytostatic;
immunosuppressive; cancer; autoimmune disease; gene therapy.
                                                                                                                 Human CD72-targeted IgG1 light chain.
                          ADR23362 standard; protein; 215
                                                                                   04-NOV-2004 (first entry)
                                                       ADR23362;
RESULT 6
               ADR23362
                                         XXXXXXXXXXXXXX
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New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders.
                                                                                                                                                                                                                       present sequence is the protein sequence of the light chain of
                                                                                                                                                                                                         Example 5; SEQ ID NO 54; 174pp; English
             Location/Qualifiers
                    1. .109
/label= V_region
110 .215
/label= C_region
                                                                                         27-JAN-2003; 2003WO-EP050004
                                                                                                       27-JAN-2003; 2003WO-EP050004
                                                                                                                      (CRUC-) CRUCELL HOLLAND BV.
                                                                                                                                      Bakker ABH, Marissen WE;
                                                                                                                                                     2004-580978/56.
                                                                                                                                                     WPI; 2004-580978/
N-PSDB; ADR23361.
                                                           WO2004067569-A1
                       Region
                                     Region
               Key
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internalising human binding molecules are capable of (specifically tecognises human B cell associated antigen CD72. An SCPV ADR23324 selected from an antibody phage display library was shown to specifically recognise the human CD72 receptor. The scrv was recloned in IgG expression vector Col using primers designed to restore complete human frameworks, thereby generating antibody 025. Such anti-CD72 immunoglobulins or their antigen-binding fragments can be used as internalising human binding molecules are capable of (specifically) binding to CD72 or its antigenic determinant, and preferably bind to CD72 associated with cells. Upon binding to CD72 present on the surface of associated with cells. Upon binding pro CD72 present on the surface of internalising human binding molecules internalise. In addition to the internalising human binding molecules, the invention provides immunoconjugates comprising an internalising human binding molecule and a immunoconjugates comprising an internalising human binding molecule and a immunoconjugates. tag (toxic substance, radioactive substance, liposome and/or enzyme), nucleic acids encoding these, and compositions comprising them. The internalising human binding molecule, immunoconjugate, nucleic acid molecule or composition can be used in the diagnosis and/or treatment of a B cell associated disorder or disease, especially a B cell associated cancer and B cell associated autoimmune disorder (claimed).

4 111 174 57 PARFSGSLIGDKAALTITGAQTEDBARYFCALWYCNL-----WVFGGGTKLTVLSRTV AAPSVFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKD SAVVTQESALTISPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV Gaps 31; Indels 16; Query Match
68.7%; Score 779; DB 8; Length 215;
Best Local Similarity 72.3%; Pred. No. 5.4e-52;
Matches 162; Conservative 15; Mismatches 31; Indels 1 STYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218 62 115 175

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to domain deleted CC49 or C2BB antibodies.

Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CL72 domain has been deleted and are reactive with tumour associated antigen (TAG3-72. The C2BB antibodies are reactive with tumour associated antigen (TAG3-72. The C2BB antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2BB construct where the CH2 domain has been deleted.

Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from neoplastic disorder such as haematologic neoplasm, preferably non-chain such as haematologic mopalsmy. They are neoplastic disorder, colon cancer and haematologic malignancy. They are useful for reducing tumour size, inhibiting tumour growth and/or prolonging the survival time of tumour-bearing animals and for treating tumours. The present sequence is human C2BB light chain protein. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel domain deleted CC49 antibody reactive with tumor associated antigen -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.
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                                                                                                                                                                                         Human, CC49 antibody, C2B8 antibody, tumour associated antigen, TAG-72, neoplasm, neoplastic disorder, haematologic neoplasm, colon cancer, non-Hodgkin's lymphoma, haematologic malignancy, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.0%; Score 759.5; DB 5; Best Local Similarity 70.5%; Pred. No. 1.9e-50; Matches 155; Conservative 16; Mismatches 42;
                                                                                                                                                     Human C2B8 antibody light chain protein.
                                   AAE27925 standard; protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chinn P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3B; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2002; 2002WO-US002373
                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-698547/75.
N-PSDB; AAD45754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braslawsky GR,
                                                                                                                                                                                                                                                                                                         WO200260955-A2
                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                 27-DEC-2002
                                                                                                                                                                                                                                                                                                                                               08-AUG-2002
                                                                           AAE27925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
RESULT 7
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monomeric subunits, where the monomeric subunits are non-covalently associated. (I) is useful for treating a disorder, especially immune disorder, and neoplastic disorder such as relapsed Hodgkin's disease, resistant Hodgkin's disease high grade, low grade and intermediate grade non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL), lymphoma (FL), diffuse large cell lymphoma (DCLL), Burkitt's lymphoma, AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic lymphomas, monocytic, follicular, diffuse small cleaved cell, large cell immunoblastic lymphoblastoma, small cleaved cell, arge cell immunoblastic lymphoblastoma, small cleaved burkitt's and non-Burkitt's, follicular, mixed small cleaved and large cell lymphoms, in a mammal (see ABZ24017 for a detailed description of the various uses of (I)). The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel dimeric antibody useful for treating immune disorder and neoplastic disorder, has several non-covalently associated monomeric subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic; vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic; thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial; neuroprotective; antipsoriatic; antintheumatic; antiarthritic; antiulcer; dermatological; immunosuppressive; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSAVVIQES--ALTISPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a dimeric antibody (I) comprising several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.0%; Score 759.5; DB 6; 70.5%; Pred. No. 1.9e-50; ive 16; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hariharan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents the antibody C2B8 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chinn P,
                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 3B; 78pp; English.
                                                                                                                                                                                                            ABB82834 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
21-DEC-2001; 2001US-0341858P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2002; 2002WO-US002374.
                                                                                                                                                                                                                                                                                                                                                     31-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Braslawsky GR, Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-140446/13.
                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody C2B8 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABZ24018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200296948-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2002;
                                                                                                                                                                                                                                                                                ABB82834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPSDEQLKSCTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSSDEQLKSGTASVVCLLMNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is used in a method for obtaining a novel gene construct (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-targeting group (I) and a heterologous prodrug-converting enzyme (II), and (B) is directed to leave the cell for selective localisation at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target site, then administration of (III) is used for targeted release of cytotoxic drug, specifically for treating cancer but also inflammation such as rheumatoid arthritis. In situ generation of the targeting antibody increases selectivity, reducing side effects at normal tissue. The method is applicable to any antibody-directed enzyme prodrug therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New gene construct expressing conjugate of targetting agent and prodrug-
converting enzyme - useful for, e.g. targetted production of cytotoxic
drug in vivo, especially for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VVTQESA-LITISPGETVTLICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                           Conjugate; cell targeting; cytotoxic drug; prodrug therapy system; prodrug-converting enzyme; cell surface antigen; treatment; cancer; inflammation; rheumatoid arthritis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.8%; Score 757; DB 2; Length 235; 71.8%; Pred. No. 3e-50; ive 15; Mismatches 40; Indels
                                            LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                Plasmid pNG3/A5B7VK-HuCK-NEO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1f; Page 70; 100pp; English
                                                                                                                                                                              AAW82740 standard; protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-GB001294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-00009421
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Emery SC, Blakey DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-059700/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV72047
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9851787-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-1997;
                                                                                                                                                                                                                                                        10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim
Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
                                                                                                                                                                                                                  AAW82740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
          118
                                            183
                                                                                  178
                                                                                                                                                                AAW82740
                                                                                                                                            RESULT
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          셤
                                            ઠે
                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 PPSDEQLKSGTASVVCLLANFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                    The invention relates to an antibody comprising an Fc variant portion having an amino acid modification in the Fc region of the parent Fc polypeptide, where the Fc variant modulates binding to an Fc-gamma-R compared to the parent Fc polypeptide. The antibody may also be used in research and in agricultural or industrial applications. This sequence corresponds to the light chain of the antibody "Rituximab" as an example
                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; antiinflammatory; cardiovascular; gene therapy; antibody; Fc; agriculture; industrial application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New optimized Fc variant antibody useful for diagnosing or treating diseases (e.g. cancer, inflammation or cardiovascular diseases), in research and in agricultural or industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doberstein SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.9%; Score 759; DB 8; Length 213; 71.8%; Pred. No. 1.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Indels
                                                                                                                            196 LSSTLTLSKADYERGHKVYACEVTHOGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Antibody "Rituximab" light chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 12; Fig 31a; 192pp; English.
                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an antibody of the invention.
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                                                                                                                                                                                                                                            ADL92471 standard; protein; 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Dang V
Vafa O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2002; 2002US-0414433P.
23-JAN-2003; 2003US-0442301P.
02-MAY-2003; 2003US-0467606P.
12-JUN-2003; 2003US-0477639P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2003; 2003WO-US030249
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                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chirino AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karki SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-316096/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004029207-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XENC-) XENCOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                         01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lazar GA,
Hayes RJ,
                                                                                                                                                                                                                                                                                  ADL92471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                          179
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Matches
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dermatitis, Crohn's disease, Graves's disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-2001; 2001EP-00112237.
26-SEP-2001; 2001US-0325147P.
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N-PSDB; AAD53214, AAD53217.
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                           Similarity
                                                                                                                                                           Sequence 235 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                                                                             Best Local Sim:
Matches 154;
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                                                                                                                                                                                            Query Match
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ID AAE3
8$888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a dimeric anti-CD20 light chain polypeptide. The dimeric immunoglobulin is used in the method of the invention. The specification describes a method for producing an immunoglobulin (Ig) G/IgG dimer. The method comprises genetically engineering a monoclonal antibody to introduce a cysteine molecule which inhibits formation of intramolecular disulphide bridges between sister heavy. Chains on the same antibody molecule. The dimer is a homodimer or heterodimer that is capable of activating components of the complement system, and has the ability to activate and kill cells via the complement cascade. The dimer is also capable of binding to Fogamma receptors or initiating programmed cell death. The IgGIGG dimers may be used to treat allergic disorders, cancers and autoinmune diseases such as allergic asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis,
                                                                                                                                                                                                                                                                                                                 complement system; Fcgamma receptor; cytotoxic effector ceil; host immune cell; programmed cell death; allergic disorder; cancer; autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease; allergic bronchopulmonary aspergillosis; allergic rhinitis; Graves's disease; food allergy; allergic contact dermatitis; cancer; becall tymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis; pigeon breeder's disease; hepatitis; leprosy; Lyme disease; disease; aplastic anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "murine anti-human CD20 variable light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               engineering immunoglobulin (Ig) G/IgG dimers for the cancers, allergic disorders and autoimmune conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "murine anti-human CD20 variable light cna
129. .235
/note= "human kappa light chain constant region"
                                                                                                                                                                                                                                                                                                  Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huynh TB;
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                                   LTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                               A dimeric anti-CD20 light chain polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 1A-B; 65pp; English.
                                                                                                                                       AAB08025 standard; protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-2000; 2000WO-US001893
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                                                                                                                                                                                                             (revised)
(first entry)
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Homo sapiens.
Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetically
                                                                                                                                                                                                           12-SEP-2003
14-NOV-2000
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                183
                                                 200
                                                                                                                                                                            AAB08025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They may also be used to treat a range of other diseases and disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected cell populations. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIWA8 antibody; heavy chain variable region; light chain variable region;
VH; VL; CD44v6; medicament; cancer; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel antibody molecules comprising a variable region of the heavy (VH) and/or light chain (VL) of CD44v6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKRWIYATSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSAVVTQES -- ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                           66.5%; Score 754.5; DB 3; Length 235; 70.0%; Pred. No. 4.6e-50; ive 16; Mismatches 43; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heider K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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breast, head and neck, ovarian and lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patzelt E, Sproll M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIWA4/8 antibody light chain mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEH ) BOEHRINGER INGELHEIM INT GMBH. (BOEH ) BOEHRINGER INGELHEIM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE34878 standard; protein; 213
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                                                                                                                                                                                                                                                                122
specific humanised antibody called BIWA8 and BIWA4. Sequences of the invention are useful for manufacturing a medicament and for treating cancer including colorectum, non-small cell lung, breast, head and neck ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BIWA48 antibody light chain mature protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                          182
                                                                                                                                                                                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of a conjugate of antibody to specified cell differentiation antigen with cytocoxic compound in the preparation of pharmaceutical composition for the treatment of cancer.
                                                                                                                                                                                                        62
                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; cell differentiation antigen-44; CD44; cytotoxic; chemotherapeutic agent; cytostatic; head; neck squamous cell carcinoma; oesophagus; lung; skin; cervix; breast adenocarcinoma; pancreas; colon; stomach; human; murine; mouse; antibody; BIWA8; light chain.
                                                                                                                                                                                                                                                               63 ARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                       4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for the preparation of a pharmaceutical composition for the treatment of cancer whereby a conjugate of a specific antibody to cell differentiation antigen-44
                                                                                                                                                                           9
                                                                                                                                              Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised murine antibody BIWA8 light chain protein.
                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                 66.4%; Score 753; DB 6; 72.2%; Pred. No. 5.4e-50;
                                                                                                                                                                                                                                                                                                                                                                                    LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                           14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL15445 standard; protein; 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heider K;
                                                                                                                                                Query Match
Best Local Similarity 72.2%
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADL15446.
                                                                                                                    Sequence 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of compound comprising antibody molecule specific for CD 44, linker moiety and compound toxic to cells, in combination with radiotherapy for preparation of pharmaceutical composition for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                    28
(CD44) with a cytotoxic compound is used optionally in combination with chemotherapeutic agent. The method of the invention has cytostatic applications and may be useful in the preparation of a pharmaceutical composition for the treatment of cancer, particularly head and neck squamous cell carcinoma, oesophagus squamous cell carcinoma, skin squamous cell carcinoma, lung adenocarcinoma, cervix squamous cell carcinoma, pancreas adenocarcinoma, colon adenocarcinoma, lung adenocarcinoma, pancreas adenocarcinoma, colon adenocarcinoma and stomach adenocarcinoma. The current sequence is that of the humanised murine antibody BIWAB light
                                                                                                                                                                                                                                                                                                                                    3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP
                                                                                                                                                                                                                                                                                                                                                                                                      59 ARPSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                 4 VVTQESA-LITSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD44 specific antibody; CD44; cancer; radiotherapy; CD446 specific antibody; maytansinoid; radioimmunotherapeutic; cytostatic; immunostimulator; head and neck squamous cell carcinoma; ossophagus squamous cell carcinoma; lung squamous cell carcinoma; skin squamous cell carcinoma; skin squamous cell carcinoma; breast adenocarcinoma; lung adenocarcinoma; pancreas adenocarcinoma; colon adenocarcinoma;
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised murine antibody BIWA 8 light chain protein SEQ ID NO:8.
                                                                                                                                                                                                                                                                   . 9
                                                                                                                                                                                                                               Score 753; DB 8; Length 213;
Pred. No. 5.4e-50;
                                                                                                                                                                                                                                                                   40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humanised murine antibody BIWA 8 light chain.
                                                                                                                                                                                                                                                                 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO00853 standard; protein; 213
                                                                                                                                                                chain protein of the invention.
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                                                                                                                                                                                                                                  66.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2002; 2002EP-00024881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                    Best Local Similarity 72.2
Matches 156; Conservative
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                                                                                                                                                                                                Sequence 213 AA;
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o sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
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Sproll M;

Patzelt E,

Heider K,

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The invention relates to a compound comprising CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions. The compound is used in pharmaceutical composition for the treatment of cancer, solid tumours, and as an adjuvant to surgical intervention to treat minimal residual disease. The present sequence is humanised murine antibody BIWA4 light chain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound useful for treatment of cancer comprises CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions.
                                                                                                                                                                                                                      (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 14; 31pp; English
                                                                                            18-MAY-2001; 2001EP-00112227.
                                                                                                                                                           18-MAY-2001; 2001EP-00112227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in the invention
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-177273/18.
N-PSDB; AAD53976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 213 AA;
                                 20-NOV-2002
                                                                                                                                                                                                                                                                                     Adolf G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                           The present invention describes using a compound (CD) of formula A(LB),
where A is an antibody molecule which is specific for CD44, L is a linker
molety, B is a compound which is toxic to cells, and n is a decimal
cumber between 1-10, for the preparation of a pharmaceutical composition
for the treatment of cancer, where CD is used or is for use in
combination with radiotherapy. Also described: (1) use of a conjugate
CC combination with radiotherapy. Also described: (1) use of a conjugate
CC combination with radiotherapy; (2) a
manufacture of a pharmaceutical composition for the treatment of cancer,
where CJ is used or is for use in combination with radiotherapy; (2) a
pharmaceutical composition. Con together with a
cradioimmunotherapeutic agent and optionally further comprising one or
more carrier(s), diluent(s), or excipient(s); (3) a kit comprising, in a
cardioimmunotherapeutic agent; and (4) use of radioimmunotherapeutic agent
cc radioimmunotherapeutic agent; and (4) use of radioimmunotherapeutic
CC reatment of cancer, where the radioimmunotherapeutic agent is used or is
CC for use in combination with CD or CJ. CD and CJ have cytostatic
cc crisein and can be used as immunostimulators. CJ is useful for the
manufacture of a medicament for the treatment of cancer e.g. head and
cneck squamous cell carcinoma, solon adenocarcinoma, pancreas
cc denocarcinoma, breast adenocarcinoma, lung adenocarcinoma, pancreas
cc denocarcinoma, colon adenocarcinoma, lung adenocarcinoma, pancreas
cc denocarcinoma, colon adenocarcinoma, lung adenocarcinoma, pancreas
cc denocarcinoma, colon adenocarcinoma, lung adenocarcinoma, colon adenocarcinoma, colon adenocarcinoma, colon adenocarcinoma, lung adenocarcinoma, colon adenocarcinoma, and stomante compensente a humanistering conterior anticherapeutic combination with r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the exemplification of the present invention.
                          Claim 7; SEQ ID NO 8; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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182 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LILSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213 7, 2005, 15:54:04 Search completed: June Job time : 115.5 secs 183 178

PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182

123

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PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST

LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218 LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 213

183 178 CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease; antigen; cytostatic; BIWA4 antibody; murine.

Homo sapiens EP1258255-A1

Humanised murine antibody BIWA4 light chain protein.

(first entry)

17-JUN-2003

BXSXXXXXXXXXXXXXX

AAE35326;

AAE35326 standard; protein; 213 AA

AAE353

177

4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP

66.2%; Score 751; DB 6; Length 213; 72.2%; Pred. No. 7.6e-50; rive 13; Mismatches 41; Indels

Similarity

58

Gaps

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Sequence Sequence Sequence Sequence

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OM protein

Run on:

Sequence:

Title: Parfect

Minimum DB Maximum DB

Database

Result Š.

Searched:

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Best Local Similarity 71.8%; Pred. No. 7.9e-67;
Matches 155; Conservative 15; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk,
US-09-453-234-74
US-09-485-737B-69
US-10-711-485-69
PCT-US-96-13152-2
US-08-630-820-6
US-09-0273-449-72
US-09-027-449-72
US-09-027-449-72
US-09-234-340A-72
US-09-121-952A-72
US-09-121-952A-72
US-09-121-952A-72
US-09-121-952A-72
US-09-121-952A-75
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US-09-026-985-56
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US-09-121-952A-56
US-09-121-952A-56
US-09-121-952A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423.439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION . cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     US-09-423-439-18
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                                              RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18,
Sequence 1, A
Sequence 1, A
                                                                                                                                                                                             1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218
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Sequence 6
Sequence 1
Sequence 2
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-472-087-15
US-09-472-087-15
US-09-472-087-67
US-09-312-926A-79
US-09-312-926A-79
US-09-472-087-67
US-09-472-087-65
US-09-472-087-65
US-09-456-090A-84
US-09-456-090A-84
US-09-456-090A-84
US-09-456-090A-84
US-09-456-090A-84
US-09-456-090A-84
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US-09-456-090A-46
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US-09-740-002-26

US-09-740-002-24

US-08-458-516-12

US-09-17-945-17

US-09-456-090A-36

US-09-453-234-36
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                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            sw model
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Gapop 10.0 , Gapext 0.5
                                                                               protein search, using
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seq length: 200000000
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1134
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Match Length
                                                                                                            June
                                                                                                                                                                                                                                                                                                Total number of
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731.5
730.5
728.5
728.5
726.5
726.5
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750
750
743
743
736
737
732
732
732
732
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                                                                                                                                                                                  score:
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Gaps

9

ARESGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122

63

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Sequence Sequence Sequence

JS-09-456-090A-74

722.5 722.5 722.5

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                                                         140 PPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEQLKSGTASVVCLLMNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187
81 ARFSGSGGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 SALTISPGETVTLICRSSIGAVTIS----NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF
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                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Indels
                                                                                                                    183 LTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                         66.1%; Score 750; DB 3; 71.8%; Pred. No. 3.6e-66; iive 13; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfratin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 02-UNM-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             Sequence 1, Application US/08952235 Patent No. 6207152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 220 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.1
Best Local Similarity 71.8
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-952-235-1
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SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 DEQLKSGTASVVCLLANFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 SALITSPGETVTLICRSSIGAVITS---NYANWVQEKPDHLFTGLIGGINNRAPGVPARF
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                                                                                             APFLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Hepatcoyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-Jul-2001
CLASSIFICATION NUMBER: US/08/952,235
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US/08/952,235
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: 08/460368
FILING DATE: 02-UUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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18-09-472-087-15
Sequence 15, Application US/09472087
Patent No. 6682736
               Sequence 1, Application US/09669971; Patent No. 6468529
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 220 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 65/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.8%
Matches 153, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
US-09-669-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-669-971-1
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64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
                                                                                                               123 PPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                 5 VTOE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVOEKPDHLFTGLIGGTNNRAPGVPA
4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                             63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B.Cell Lymphoma and Cell Line
CORRESPONDENCE: 14
CORRESPONDENCE: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.2%; Score 739; DB 3; Length 213; 70.7%; Pred. No. 4.2e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/397,411
                                                                                                                                                                                                                                                                 183 LTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                            Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 011823-0049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 12, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 213 amino acids
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Best Local Similarity 70.7%
Matches 152; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-08-397-411-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 PPSDEQLKSGTASVVCLLANFYPREAKVOMKVDNALQSGNSQESVTEQDSKDSTYSLSST 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NUEUU, MARK J.
APPLICANT: MUSULER, EILLEN E.
APPLICANT: MUSULER, EILLEN E.
APPLICANT: CANTAIN, JEFREY H.
APPLICANT: CONVALN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPRENCE: ABX-PPI
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR PLICATION NUMBER: 60/113,647
PRIOR PLICATION NUMBER: 60/113,647
PRIOR PLICATION UNDER: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 67
LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.5%; Score 743; DB 4; Length 233; 70.4%; Pred. No. 1.9e-65; ive 19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.5%; Score 743; DB 4; Length 23 Best Local Similarity 70.4%; Pred. No. 1.9e-65; Matches 152; Conservative 19; Mismatches 39; Indels
                    APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, BILLERN B.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFRENCE: ABX PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233
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                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 233
LENGTH: 233
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Patent No. 6682736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-09-472-087-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 152; Conserv
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US-09-472-087-67
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EKHKVYACEVTHOGLSSPVTKSFNRGEC 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 72.6%
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-315-926A-79
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63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 SRFSGSGSGTDYTLTISSLÓPEDIATYYCOHWSSKPPTFGGGTKVEV-KRTVAAPSVFIF 139
                                                        PSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 VLTQSPSSLSVSVGDRVTMTCRAS----SSVTYIHWYQQKPGLAPKSWIYATSNLASGVP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.9%; Score 736; DB 4; Length 235; 70.8%; Pred. No. 9.4e-65; Live 15; Mismatches 42; Indels
                                                                                                                              184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                       179 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pillsbury Madison & Sutro,
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION AUNABRE: CT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 15-AUG-1995
INFORMATION FOR SEQ 1D NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                       HENNEQUIN, Laurent F.A.
MARSHAM, Peter R.
DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-011-769A-27
                                                                                                                                                                                                                                                          Sequence 27, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
BLAKEY, David C.
DAVIES, David H.
HENNAM, John F.
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Best Local Similarity
Matches 153; Conserva
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US-09-011-769A-27
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Sequence 79, Application US/09315926A

Patent No. 6498027

GENERAL INFORMATION:

APPLICANT: Bavenga, Menzo

APPLICANT: Havenga, Menzo

APPLICANT: Havenga, Menzo

APPLICANT: Havenga, Menzo

APPLICANT: Verlinden, Stefan

TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

FILE REFERENCE: 2183-4080US

CURRENT APPLICATION NUMBER: EP 99201593.3

PRIOR APPLICATION NUMBER: EP 99201693.3

PRIOR FILING DATE: 1998-05-20

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 81

SOCTWARE: PATENT VERSION 3.0

SEQ ID NO 79

LENGTH: 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
OTHER INFORMATION: Description of Artificial Sequence: phage
NAME/KEY: PEPTIDE
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, MARK J.
APPLICANT: MUSLLER, EILLEN E.
APPLICANT: HANKE, JEFREY H.
APPLICANT: HANKE, GEOFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)..(236)
OTHER INFORMATION: /note="hCAT1 amino acid sequence'
                                LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198
                                                                                                                               199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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Matches 150; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ARPSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 234;
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GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NUEVEU, MARK J.
APPLICANT: NUEVEU, MARK J.
APPLICANT: GILMAN, STEVEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 06/113,647
PRIOR PILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATCHIN UNCS: 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 732.5; DB 4
Pred. No. 2.1e-64;
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                     CURRENT APPLICATION NUMBER: US/09/472,087
                                           CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 69, Application US/09472087
Patent No. 6682736
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Best Local Similarity 69.9%;
Matches 151; Conservative 1
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Best Local Similarity 69.9%
Matches 151; Conservative
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ORGANISM: Homo sapiens
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US-09-472-087-69
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140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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Sequence 14, Application US/09472087

Sequence 14, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, MARK J.
APPLICANT: HANNE, EILLEN E.
APPLICANT: HANNE, STEVEN C.
APPLICANT: GEOFFREY H.
APPLICANT: GEOFFREY H.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 60/113,647

PRIOR APPLICATION NUMBER: 60/113,647

PRIOR PILING DATE: 1999-12-23

PRIOR PILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14

LEMATOR.
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Sequence 65, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: MUELLER, BILLEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
IILE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR PADLICATION DATE: 1999-12-23

WINDOW FILING DATE: 1998-12-23
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Sequence 84, Application US/09453234
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                                                                                                                               Query Match 64.6%; Score 732; DB 4; Length 235; Best Local Similarity 69.4%; Pred. No. 2.3e-64; Matches 150; Conservative 19; Mismatches 43; Indels
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APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
ATITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 71.4%; Pred. No. 2.5e-64;
Matches 155; Conservative 14; Mismatches 39; Indels
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 SOFTWARE: Patentin Ver. 2.1
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OCGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84
                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-09-453-234-84
                 SEQ ID NO 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4%; Pred. No. 2.5e-
Matches 155; Conservative 14; Mismatches
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Fatent No. 6828121
GENERAL INFORMATION:
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT RPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR PILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
                                                              APPLICANT: Valkirs, Gunars
APPLICANT: Valkirs, Gunars
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE REPRENCE: 020015-000110US
CURRENT FILIOR DATE: 1999-12-01
CURRENT FILIOR DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 84
LENGTH: 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens; OTHER INFORMATION: M2-32L
US-09-453-234-84
Patent No. 6794132
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Patent No. 6828121
US-10-011-125A-2
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21: /cgn2_6/ptodata/1/pubpaa/US106_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                 Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

# Result Ouery B ID Description No. Score Match Length DB ID Description 2 1083 95.5 218 16 US-10-625-047-27 Sequence 27, Appl 2 1083 95.5 218 16 US-10-723-003-42 Sequence 28, Appl 3 759.5 67.0 235 16 US-10-723-003-42 Sequence 28, Appl 5 753 66.4 213 14 US-10-150-475A-8 Sequence 8, Appl 6 753 66.4 213 16 US-10-704-522-8 Sequence 8, Appl 7 751 66.2 213 16 US-10-704-522-8 Sequence 8, Appl 8 Appl 1 8 751 66.2 213 16 US-10-704-522-4 Sequence 4, Appl 1 1 750 66.1 220 9 US-09-995-633-1 Sequence 1, Appl 1 1 750 66.1 220 14 US-10-24-06-1 Sequence 1, Appl 1 1 750 66.1 220 14 US-10-22-406-1 Sequence 1, Appl 1 1 750 66.1 220 14 US-10-22-406-1 Sequence 1, Appl 1 1 750 65.1 213 15 US-10-22-406-1 Sequence 1, Appl 1 1 750 65.1 213 15 US-10-22-406-1 Sequence 12, Appl 1 1 750 65.1 213 15 US-10-22-406-1

115 743.5 65.6 234 10 US-09-888-832-4 Sequence 1, Maria 15 65.6 1	Sequence 4, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 15, Appli Sequence 67, Appl Sequence 67, Appl Sequence 122, Appl Sequence 122, Appl Sequence 124, Appl Sequence 106, Appl Sequence 106, Appl Sequence 17, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 17, Appl Sequence 129, Appl Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18,	fornia  pence:native cloned formin wariable region formin wariable region formin forcin forci
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US-10-150-475A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:N53C cloned CHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable OTHER INFORMATION: region (VL) fused to human anti-teranus toxin OTHER INFORMATION: antibody kappa light chain constant region (TTCL) US-10-625-047-28
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Publication No. US20040254108A1
GENERAL INFORMATION:
APPLICANT: MA, Jinn
APPLICANT: GUO, Yajun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003
                                                                                                                                                                                                                                                                                      US-10-625-047-28

Sequence 28, Application US/10625047

Publication No. US20040198962A1

Publication No. US20040198962A1

SENERAL INFORMATION:

APPLICANT: Meares, Claude

APPLICANT: The Regents of the University of California

TILE OF INVENTION: Multi-Functional Antibodies

FILE REFERENCE: 023070-130910US

CURRENT APPLICATION NUMBER: US/10/625,047

CURRENT FILING DATE: 2003-07-22

PRIOR FILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28

LENGTH: 218
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Best Local Similarity 95.9%; Pred. No. 1.3e-84;
Matches 209; Conservative 0; Mismatches 9
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US-10-723-003-42
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                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REPRENCE: 1/1211
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT FILING DATE: 2002-05-17
PRIOR PILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
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PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR FILING DATE: 2003-11-25
PRIOR PPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
ERG ID NO 42
LENGTH: 235
                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/10150475A, Publication No. US20030103985A1; GENERAL INFORMATION:
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 156; Conservative
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US-10-150-475A-4
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GENERAL INFORMATION:

APPLICANT: Adolf, Guenther:

APPLICANT: Baum, Anke

APPLICANT: Baum, Anke

APPLICANT: Baum, Anke

TITLE OF INVENTION: Compositions and Methods for Treating Cancer using;

TITLE OF INVENTION: Chemotherapeutic Agents

TITLE OF INVENTION UNMBER: US/10/645,215

CURRENT PILING DATE: 2003-08-21

PRIOR FILING DATE: August 21, 2002

PRIOR PILING DATE: August 26, 2002

WUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Baumann, Michael
APPLICANT: Baumann, Michael
APPLICANT: Heider, Karl-Heinz
APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and methods for treating cancer using
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
TITLE OF INVENTION OF COMPARE: US/10/704,522
CURRENT APPLICATION NUMBER: US 60/429,516
PRIOR APPLICATION NUMBER: EP 02024881
PRIOR FILING DATE: 2002-11-27
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NOS: 9
SET OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.4%; Score 753; DB Best Local Similarity 72.2%; Pred. No. 1.9e-Matches 156; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10645215
Publication No. US20040126379A1
                                                                                                                                                                                                                                       Sequence 8, Application US/10704522 Publication No. US20040120949A1
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                                                                                                                                                                                                                                      9
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                                                                                                                                                                                         Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10150475A
Publication No. US20030103985A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REPRENCE: 1/1211
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT APPLICATION NUMBER: US 60/307,451
PRIOR APPLICATION NUMBER: US 60/307,451
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                    Indels
                                                                                                                ; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain US-10-645-215-8
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                                                                                                                                                                  66.4%; Score 753; DB 16;
Best Local Similarity 72.2%; Pred. No. 1.9e-56;
Matches 156; Conservative 14; Mismat-1.
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 72.21
Matches 156; Conservative
SOFTWARE: Patentin Ver.
SEQ ID NO 8
LENGTH: 213
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FEATURE:
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Sequence 4, Application US/10645215

Sequence 6, Application US/10645215

Sequence 7, Application US/10645215

Sequence 8, Application Wo. US20040126379A1

Sequence 8, Application Wo. US20040126379A1

APPLICANT: Baum, Anke

APPLICANT: Baum, Anke

APPLICANT: Heider, Karl-Heinz

TITLE OF INVENTION: Compositions and Methods for Treating Cancer using

TITLE OF INVENTION: Cycloxic CD44 Antibody Immunoconjugates and

TITLE OF INVENTION: Chemotherapeutic Agents

FILE REFERENCE: 1/1383

CURRENT FILING DATE: 2003-08-21

PRIOR FILING DATE: 2003-08-21

PRIOR PPLICATION NUMBER: EP 02 018 686.2

PRIOR PLING DATE: August 21, 2002

PRIOR PAPLICATION NUMBER: US 60/405,956

PRIOR PLING DATE: August 26, 2002

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 4

LENTH: 213
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                                                  Sequence 4, Application US/10704522

Publication No. US20040120949A1

GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Heider, Karl-Heinz
ITILE OF INVENTION: Compositions and methods for
TITLE OF INVENTION: Compositions and methods for
TITLE OF INVENTION: Compositions and methods for
TITLE OF INVENTION: COMPOSITION and methods for
FILE REFERENCE: 1/1414
CURRENT APPLICATION NUMBER: US/10/704,522
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: US 60/429,516
FRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTING UNC: 2.1
SEQ ID NO 4
LENGTH: 213
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain US-10-645-215-4
                                                                                    66.2%; Score 751; DB 16; Length 213; larity 72.2%; Pred. No. 2.8e-56; Conservative 13; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/995,693
FILING DATE: 29-No. US20020136721A1-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/952,235
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Genethech, Inc.
STREET: I DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09995693; Patent No. US20020136721A1; GENERAL INFORMATION: APPLICANT: Schwall, Ralph H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650/225-5416
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
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                                                                                                              Best Local Similarity
Matches 156; Conserv
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Sequence 4, Application US/09848832
Publication No. US20030165507A1
GENERAL INFORMATION:
APPLICANT: Hooper, Dietzschold, Bernhard
TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
TITLE OF INVENTION: ADMINISTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
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SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
                      DEQLKSGTASVVCLLMNPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                                                                         5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
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US-10-435-299-12
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Sequence 12, Application US/10435299
Publication No. US2004005278341
GENERAL INFORMATION:
APPLICANT: Weater, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Gingrich, Roger
APPLICANT: Gingrich, Roger
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
FILE REPERENCE: 05882-017-6-CNUS04
CURRENT APPLICATION NUMBER: US/10/435,299
CURRENT FILING DATE: 2000-07-18
FRIOR FILING DATE: 1995-03-01
FRIOR PELLING DATE: 1995-03-01
FRIOR FILING DATE: 1995-03-01
FRIOR FILING DATE: 1992-03-07
SPIOR FILING DATE: 1992-03-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE PRECEDIATION NUMBER: US 07/859,583
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.7%; Score 745; DB 15; 71.2%; Pred. No. 9.1e-56; ive 16; Mismatches 40;
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Best Local Similarity 71.2*
Matches 153; Conservative
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                                                                                                     128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTXSLSSTLTL 187
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                            SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS
         SALTISPGETVILICRSSIGAVITS ---NYANWVQEKPDHLFIGLIGGINNRAPGVPARF
                                                                                                                                                 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.1%; Score 750; DB 14; Length 220; Best Local Similarity 71.8%; Pred. No. 3.5e-56; Matches 153; Conservative 13; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 SKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 220
                                                                                                                                                                                                                         SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P0938P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 220 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10232408
Publication No. US20030118587A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                  PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                             139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 ARFSGSGSGTDFTLSISSLEPEDFAVYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVPIF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 VLTQSPATLSLSPGERATLACKAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79
                                                                                                                                                                                                                                       4 VVTQESA-LITSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                                                                                                                                                                Length 234;
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Them
                                                                                                                                                                                                            44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels
                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                    183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                                                                              65.6%; Score 743.5; DB 1.
71.8%; Pred. No. 1.4e-55;
:ive 12; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.6%; Score 743.5; DB 1
71.8%; Pred. No. 1.4e-55;
iive 12; Mismatches 44
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CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                              Query Match
Best Local Similarity 71.8<sup>3</sup>
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.8°
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                      TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-225-108A-4
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                                                                                                        LENGTH: 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP
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US-10-46-148-3

US-10-46-148-3

US-10-48-3

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                                                                                                                                                                         199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
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us-09-671-953b-7.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 7, 2005, 15:39:10 ; Search time 25 Seconds (without alignments) 839.010 Million cell updates/sec

US-09-671-953B-7 1134 1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	kappa chain	kappa c	lambda	kappa chain	kappa chain		JC-kappa protein -	chain	pelB leader/Ig hea	Ig kappa chain C r	Ig lambda chain V	_	lambda	kappa c	lambda	lambda	lambda	lambda	kappa	kappa	kappa chain	kappa	kappa chain	kappa ch	lambda-	lambda ch	a-2 cha	kappa	Ig kappa chain V r
	ΔI	JE0242	JE0244	PC4156	JE0243	JE0241	A23746	S52059	S06084	PC4402	КЗНО	S52450	A31790	L1MS4E	S25058	806819	S06818	S20654	806820	S38865	S37484	A37927	S14237	S26653	533161	B54256	806822	L2MS35	868212	S68241
	B	8	N	~	N	N	~	~	7	4	-	~	~	ч	~	7	N	~	~	~	~	N	~	~	~	~	7	Н	~	7
	Match Length	215	215	214	215	216	215	135	240	287	106	128	220	129	235	113	112	106	114	219	225	66	234	66	230	113	114	129	214	218
* Ouery	Match	65.2	64.8	64.2	63.6	59.8	59.3	51.0	48.5	48.3	48.0	47.7	47.1	47.0	46.4	46.3	46.2	45.9	45.3	45.1	45.1	44.9	44.5	44.4	44.3	44.1	44.0	43.9	43.9	43.9
	Score	739	735	728.5	72	678.5	672	578.5	549.5	547.5	544	541	534.5	533	526	525	523.5	521	513.5	511	511	509	504.5	503	502.5	200	499.5	498	497.5	497.5
Result	No.	-	7	e	4	'n	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig kappa chain pre Ig kappa chain pre	monoclonal antibod	Ig kappa chain - m	Ig lambda chain V	Ig kappa chain V r	Ig lambda chain V	Ig lambda chain V	Ig lambda chain -	Ig kappa chain (mo	Ig lambda chain V	Ig lambda-1 chain	Ig kappa chain - m	Ig lambda chain V	Ig lambda chain V	Ig kappa chain V r
JL0029 S01320	JC5810	S42772	PH1089	S16112	S14582	S06821	S25749	PC4203	PH1090	LIMSV	S52028	S14584	PH1088	A56169
0 0	7	~	7	7	~	N	~	~	N	-	7	~	7	~
225	218	217	66	219	66	113	235	219	97	116	219	66	100	210
7	4	N	_	0	σ	0	80	7	Ŋ	N	Ŋ	7	7	4
43.7	43.	43.	43.	43.	42.	42.	42.	42.	42	42.	42	41.	41.	41
495.5	492.5	490	488.5	488	486	486	485	484.5	478	478	478	473	473	469.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1	
JE0242 Ig kappa chain NIG26 precursor	IG26 precursor - human
C;Species: Homo sapiens (man)	
C,Date: 05-Dec-1	C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Accession: JE0242	242 242 - The Control of Control
R; Allm, M.A.; Ya	K!Allm, M.A.; Yamaki, S.; Hobballi, M.S.; Iakeda, N.; Kojima, M.; Aakedii, F.; Aakedii, F.; Aakedii, A.; Aakedii, Aakedi
A:Description: S	submitted to orthogonal structure melationship of kappatype light chains with AL amyloide A. Description: Structure melationship of kappatype light chains with AL amyloide
A; Reference number: JE0241	er: JE0241
A, Accession: JE0242	242
A;Molecule type: protein	protein
C;Superfamily: 1	C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain:	F;16-91/Domain: immunoglobulin homology <imm></imm>
Query Match	
Best Local Similarity Matches 152; Conserv	/0.4%; /ative 1
0y 4 W	VVTQB-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
Dp 3 VL	:    :        :       :
Qy 63 AR	63 ARFSGSLIGDKAALTITGAQTEDBARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
13	
1	
Qy 123 PP	PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
120 PP	PPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
Qy 183 LT	LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
11 0B1 da	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215

osis: Mul

hinoda,

# RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

G/Species: Homo sapiens (man)

C/Species: Homo sapiens (man)

R/Alim, M.A.; Hara, N.Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

R/Alim, M.A.; Hara, N.Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

R/Alim, M.A.; Hara, N.Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

A/Hosorite to JIPID, November 1998

A/Hosorite to JIPID, November 1998

A/Hosorite type: protein

A/Hosorite type: protein

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/16-90/Domain: immunoglobulin homology <IMM>

N

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A, Molecule type: protein
                                                                                                       Similarity
                                                                                        Query Match
Best Local Simil
Matches 153; C
                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
PC4156
Ig lambda chain V region MabB23 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: D-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4156
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a A;Reference number: PC4155
A;Accession: PC4156
A;Accession: PC4156
A;Accession: PC4156
A;Accession: PC4156
A;Accession: PC4156
A;Cross-references: GB:U28967; NID:g1262178; PIDN:AAC52488.1; PID:g1262179
C;Superfantly: Immunoglobulin V region; immunoglobulin homology
F;1-214/Product: light chain #status predicted <AMT>
F;98-110/Region: V region
F;130-198/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a
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Ig kappa chain NIC93 precursor - human
G.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Accession: JE0248
S.A. Hara, Y. Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, submitted to JIPID, November 1998
A.Pascription: A new subgroup of k type light chains (VkV) identified in cases of A.Reference number: JE0243
A.Reference number: JE0243
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                                                                                                                                                                ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLW---VFGGGTKLTVLSRTVAAPSV 119
                                                                                                                                                                                                   ARFSGSGSGTDF1LT1SSLQSEDFALYYCQQY--NTWPPLTFGGGTKVEI-KRTVAAFSV 116
                                                                                                                                                                                                                                         FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                              ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST--YSLS 180
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                                                                                        4 VVTQESA-LITSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                                      Gaps
                                                      10;
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               Length 215;
             Query Match 64.8%; Score 735; DB 2; Length 21: Best Local Similarity 71.7%; Pred. No. 2.9e-48; Matches 157; Conservative 13; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                     SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
                                                                                                                                                                                                                                                                                                                   SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.2%; Score 728.5; DB 2 66.5%; Pred. No. 8.8e-48; ive 23; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 145; Conservative
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C.Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;All M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul.
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Ig kappa chain V-III (KAU cold agglutinin) - human

Ig kappa chain V-III (KAU cold agglutinin) - human

Ig kappa chain V-III (KAU cold agglutinin) - human

C;Species Homo sapiens (man)

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000

C;Accession: A23746

G;Accession: A23746

J; Edoni, J.; Gilso, J.; Goni, F.; Frangione, B.

J; Biol. Chem. 266, 2836-2842, 1991

A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl.

A;Reference number: A23746; MUID:91131575; PMID:1993660
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                                                                                                                                                                                                                                                                                                                                                                                           ARFSGSGSGTEFTLTISSLQSEDFAIYYCQ--HNNAWPPTFGQGTKVETKRRTVAAPSVF 117
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                                                                                                                                                                                                                                        4 VVTQESA-LITSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-216 <ALI-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
A;Residues: 1.215 chir>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                 45; Indels
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                                                                                                                    Score 721; DB 2;
Pred. No. 3.2e-47;
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                                                                                                                                                                              12; Mismatches
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                                                                                                          63.65.
                                                                                                                                                                                 Conservative
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A;Accession: JE0241
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Gaps

2

82

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pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein C; Species: synthetic C; Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998 C; Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998 R; Suzuki, C; Ucda, H.; Suzuki, B.; Nagamune, T. J. Biochem. 122, 322-329, 1997 B; A; Title: Construction, bacterial expression, and characterization of hapten-specific sin A; Reference number: PC4402 PC4402
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C;Species: Homo sapiens (man)
C;Date: 31.-Dec-1980 #sequence revision 02-Jul-1998 #text change 09-Jul-2004
C;Accession: B9562; A9161; A90806; A94417; A91639; A92047; A9422; B37927; A02116; S0
R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAP---- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 FIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                         GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                     142 SIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 KDDAKKDDAKKDGQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEW
                                                                                                                                                                                                                                                                                                                                           23. VATQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGQSPKLLIYWASTRQS
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A; Molecule type: mRNA
A; Residues: 1-240 <CRO>
A; Residues: 1-240 <CRO>
A; Residues: 1-240 <CRO>
CRO>
C; Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C; Cross-references: Embl.X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C; Reywords: heterotetramer; immunoglobulin
C; Reywords: heterotetramer; immunoglobulin
F; 1.20/Domain: algnal sequence #status predicted <SIG>
F; 21.240/Product: Ig kappa chain #status predicted <MAT>
F; 1.227/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                   Length 240;
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Pred. No. 4.7e-34;
                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                 48.5%; Score 549.5; DB 2
53.4%; Pred. No. 2.7e-34;
iive 24; Mismatches 73
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                                                                                                                                                                                                                                               Best Local Similarity 53.4%;
Matches 117; Conservative 2
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A; Residues: 1-287 <SUZ>
C; Keywords: fusion protein
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
N;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNP A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: S52059
R;Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S. EMBO J. 13, 5937-5943, 1994
A;Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy A;Reference number: S52059; MUID:95112804; PMID:7813432
A;Accession: S52059
A;Accession: S52059
A;Accession: S52059
A;Accession: S52059
C;Superfamily: pre-B cell omega light chain; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                             ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                        PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 PPSDEQLKSGTASVVGLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
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                                                                                                                                                                                                                                                                                                                                             VITOSPATISISPGERATISGGAS -- OSVSSNYLAWYQOKPGQAPRILIYDASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .Species: Homo sapiens (man)
.Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKS
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                 A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 rotosin
A;Residues: 1-215 rotosin
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                       Length 215;
                                                                                                                                                                                                  Query Match 59.3%; Score 672; DB 2; Length 21 Best Local Similarity 68.4%; Pred. No. 1.5e-43; Matches 147; Conservative 16; Mismatches 48; Indels
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Best Local Similarity 89.7%;
Matches 113; Conservative
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Best Local Similarity 96.3
Matches 104; Conservative
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A; Residues: 1-128 <BER>
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                                                                                                                 C;Genetics:
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A; Residues: 8-106 < KUR>
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A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
                                                                                                                                                                                                                                     A,Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
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submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
A;Reference number: S52445
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C.Accession: A31790
R.Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
R.Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
A.Title. Chem. 253, 17100-17105, 1998
A.Title. Preliminary crystallographic data, primary sequence, and binding data for an an A.Reference number: A92686; MUID:89034213; PMID:3182835
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C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
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Pred. No. 6.2e-34;
0; Mismatches 4; Indels
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                                                                                                                                                                A;Gene: GDB:IGKC
A;Cross-references: GDB:120088; OMIM:147200
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96.38;
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Conservative
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C;Species: Mus מוארמיויים ואני
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C;Complex: A' immunoglobulin heterotetramer subunit consists of two identical light (ka. hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l (;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; pyroglutamic acid F;1-19/Domain: signal sequence #status experimental <SIG>F;20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>F;34-111/Domain: immunoglobulin homology <IMM>F;20/Modified site: pyrolidone carboxylic acid (Gln) (in mature form) #status experiment F;11-109/Disulfide bonds: #status predicted
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                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-43, T', 45-50, 'G', 52-58, 'E', 60-89, 'D', 91-129 <BER>
A; Residues: 1-43, T', 45-50, 'G', 52-58, 'E', 60-89, 'D', 91-129 <BER>
A; Note: the sequence was determined from the differentiated gene
R; Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore,
Nature 298, 380-382, 1982
Nature 298, 380-380, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic
A;Reference number: A90780; MUID:79084170; PMID:103630
A;Contents: H2020
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop s A;Reference number: S25057
A;Accession: S25058
A;Steaus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Residues: 1.58,'E',60-89,'D',91-98,'T',100-105,'M',107-129 <BO' A.Note: the sequence was determined from the differentiated gene C.Comment: The MOPC 104E sequence is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 129;
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50.5%; Pred. No. 1.6e-32;
ilve 29; Mismatches 72.
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Pred. No. 2.5e-33;
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Best Local Similarity 94.4%;
Matches 102; Conservative
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Matches 109; Conservative
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A;Residues: 1-235 <FIS>
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A; Molecule type: DNA
                                                                                                                                                                                  A; Accession: A90780
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: S43
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C; Species: Mus musculus (house mouse)
C; Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
C; Accession: B93815; B93775; G93775; A93784; B93784; C93784; A90780; C93282; A01995
R; Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A; Titler Amino acid sequence of the NH-2-terminal extra piece segments of the precursors A; Reference number: A93815; MUID:77148916; PMID:403522
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                                                             A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
G;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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A;Residues: 20-43,'N',45-70,'N',72-115,'R',117-129 <CE3>
A;Note: these proteins were isolated from serum or urine of tumor-bearing
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R;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; MUD:71107854; PMID:5276767
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Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda-chain sequences.
A;Reference number: A93784; MUID:73229669; PMID:4516208
                                                                                                                                                                                                                                                                                Query Match
47.1%; Score 534.5; DB 2;
Best Local Similarity 51.6%; Pred. No. 3.4e-33;
Matches 113; Conservative 26; Mismatches 75;
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A;Residues: 'Z', 21-25,'Q', 27-129 <APP>
A;Accession: C93775
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Residues: 20-129 <CE2>
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A;Residues: 1-29 <BUR>
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                                      A; Accession: A31790
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RESULT 15
S06819
Ig lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: 806819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Titler Comparative sequence and immunochemical analyses of murine monoclonal anti-morg A;Reference number: 806815; MUID:90064531; PMID:255519
A;Accession: 806819
A;Accession: 806819
A;Accession: S06819
A;Accession: S06819
A;Accession: I-113 <AMLb
A;Residues: 1-113 <AMLb
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology <IMM>F;21-89/Disulfide bonds: #status predicted
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0; Gaps
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Best Local Similarity 94.4%; Pred. No. 8.6e-33;
Matches 102; Conservative 1; Mismatches 5; Indels
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Search completed: June 7, 2005, 16:01:08 Job time : 26 secs

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

REMBL, BC073792; AA473792.1; -.

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REMART; SM00407; IS.

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A Straubberg R.L., Feingold E.A., Grouse L.H., Ospengas. 13.000003;
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A plactenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B capleton M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,
B Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Richards S., Worley K.C., Hale S., Garcinarane P.H.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
B Richards S., Worley K.C., Hale S., Garcinard G.G.,
B Richards S., Sancher A., Sodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
A Nones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                63 ARFSGSLIGDKAALTITGAQTEDEARYFCAL---WYCNLWVFGGGTKLTVLSRTVAAPSV 119
                                                                                                                                                                                                     FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                   79
                                                                                                             4 VVTQESA-LITSPGETVTLICRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                    Gaps
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Catarrhini; Hominidae; Homo.
                                                                    10;
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                                          Length 235;
                                     Query Match
64.6%; Score 732; DB 2; Length 23
Best Local Similarity 70.3%; Pred. No. Se-56;
Matches 154; Conservative 16; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ databases
Hypothetical protein.
SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;
                                                                                                                                                                                                                                                         SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                       SSTLTLSKADYEKHVYACEVTHQGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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INTERPRO; IPRO03599; IG.
INTERPRO; IPR003597; IG-like.
INTERPRO; IPR003597; IG-C.
INTERPRO; IPR003506; IG-MHC.
INTERPRO; IPR003596; IG-V.
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Mammalia; Eutheria; Primates;
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Submitted (0CT-2001) to the
EMBL; BC016380; AAH16380.1;
HSSP; P01837; 1KCU.
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              · SEQUENCE
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TISSUE-Spleen;

XX MEDINE-25918825;

XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Hilalon B., Yetteman M., Madan A., Rodrigues S., Sanchez A.,

X Hilalon M., Touchman J.W., Green E.D., Dickson M.C.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

X Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

X Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDI-KRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 VLTQSPATLSLSPGERATLSCRAS--QIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                  Length 235;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073191; AAH73791.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
SMART; SM00409; IG; 2.
SMART; SM004015; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00239; IG_MHC; UNKNOWN_1.
PROCHELICAL protein.
SEQUENCE 235 AA; 25520 WW; F33A145A396BA285 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                              Query Match 64.5%; Score 731; DB 2; Best Local Similarity 69.9%; Pred. No. 6.1e-56; Matches 151; Conservative 19; Mismatches 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Homo sapiens (Human).
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119
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                                                                                SEQUENCE
                                                                                              Query Match
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Q7Z3Y4;
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                                                                                                                  21 RCAIQMTQSPSSLSASVGDRVTITCRASQG---ISNDLGWYQQKPGKAPKLLIYAASSLQ 77
                                                                                                                                   59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                              Gaps
                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                               . 9
                                                                                  Length 236;
                                                                                               Indels
                                                               Hypothetical protein. SEQUENCE 236 AA, 25751 MW; 5BFE6A087AFAC437 CRC64;
                                                                                                                                                                                        218
                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                         LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                 Query Match 64.2%; Score 728; DB 2; L4
Best Local Similarity 70.0%; Pred. No. 1.1e-55;
Matches 154; Conservative 15; Mismatches 45;
                                                                                                                                                                                                                                                   Created)
                                                 PROSITE; PS00835; IG_LIKB; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP007654; C1-8et; I.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0MR-2004 (TrEMBLrel. 26, Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                      PRELIMINARY;
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CTISSUE=Skeletal Muscle;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L.; Feingold B.A.; Grouse L.H.; Derga J.G.;

RIJUSHORE R.D.; Collins F.S.; Wagner L., Shenmen C.M.; Schuler G.D.;

A Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Altschul S.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haith F.;

A Detchenko L.; Marusina K.R.; Farmer A.A.; Rubin G.M.; Hong L.;

A Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schetz T.E.;

Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

Richards S., Worley K.C.; Hale S., Garcia A.M.; Gay L.J.; Hulyk S.W.;

A Nilalon D.K.; Muzny D.M.; Sodergren B.J.; Lu X.; Gibbs R.A.;

Rahesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Rayinski M.I.; Skalska U.; Smailus D.E.; Schnerch A.; Schein J.E.;

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : : | | : : | | : | | : | | : | | : | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Straugherg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO56256; AAH56256.1; -.
HSSP; PO1034; IHEZ.
InterPro; IPR0075110; Ig-1ike.
InterPro; IPR003506; Ig-MHC.
InterPro; IPR003506; Ig-WHC.
InterPro; IPR003596; Ig-V.
Pfam; PF07654; Cl-set; 1.
SMART; SMO0406; IG-V.
PROSITE; PS00230; IG-MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 725; DB 2;
; Pred. No. 2e-55;
19; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 68.2
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Strausberg R
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Altachnels C. Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bahar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bahar N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Hang J., Hsieh F.,

A papleron M., Soarse M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tocahlyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Tocahlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wokernan K.J., Malek J.A., Gunstene P.H.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raberstey R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,

A Norse S.J., Marra M.A.,

Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VTQE-SALTISPGETVILICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVPA 63
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.7%; Score 722.5; DB 2; Length Best Local Similarity 70.2%; Pred. No. 3.4e-55; Matches 15; Conservative 15; Mismatches 44; Indels
                                                                     Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_MC.
InterPro; IPR003596; Ig_MC.
Pfam; PF07654; C1-set; I.
PR0031E; PS00406; IGV.
PROSITE; PS00406; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                      EMBL; BC005332; AAH05332.1; -. HSSP; P01834; 1HEZ.
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SEQUENCE FROM N.A.
TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
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140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

A Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

B Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

B Bosak S.A., McKenn P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 VLTGSPGTLSLSPGERAALSCRAS--QSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ARFSGSLIGDKAALTIIGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.6%; Score 721; DB 2; Length 235; Best Local Similarity 69.4%; Pred. No. 4.6e-55; Matches 150; Conservative 15; Mismatches 47; Indels
                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
REDUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                           Submitted (JUN-2004) to the EMBL; BC073793; AAH73793.1;
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF07654, C1-86t, 1.
Pfam; PF00047; 1g; 2.
SMART, SM00409; IG; 2.
SMART; SW00407; IGc1; 1.
SMART; SW00406; IGv1.
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Homo sapiens (Human).
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                                                             SEQUENCE FROM N.A.
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122

62 80

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124 PSDEQLKSGTASVVCLLANFYPRAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 LTQSPSFLSASVGDRVTITCRASQG---ISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VTQE-SALITISPGETVTLICRSSIGAVITISNYANWVQEKPDHLFTGLIGGINNRAPGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 236;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO34141; AAH34141.1; -.
HSSP; P01607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 720.5; DB 2
; Pred. No. 5.1e-55;
15; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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INCEPPO: JPR001359; IG.
INCEPPO: JPR00110; IG-11ke.
INCEPPO: JPR003597; IG_C1.
INCEPPO: JPR003597; IG_C1.
INCEPPO: JPR003596; IG_WC.
INCEPPO: JPR003596; IG_WC.
INCEPPO: JPR003596; IG_WC.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
FR031TE; PS0085; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                             and mouse cDNA sequences."
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                 TISSUE=Lung;
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Q6P5S8
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetev K.H., Schaefer C.F., Bhat N.K.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                             Straubberg R.;
Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073763; AA473763.1; -.
R InterPro; IPR001399; Ig.
R InterPro; IPR001399; Ig.
R InterPro; IPR003999; Ig.
R InterPro; IPR003999; Ig.
R InterPro; IPR003999; Ig.
R InterPro; IPR003996; Ig.
R EMBL; BC0764; Ig.
R Pfam; PP07654; Cl.set; l.
R Pfam; PP07654; Cl.set; l.
R R SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
R R SMART; SM00409; IG; 1.
R PROSITE; PS50835; IG LIKE; 2.
R PROSITE; PS50835; IG LIKE; 2.
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SROUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
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Last annotation update)
                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 720.5; DB 2; 69.3%; Pred. No. 5.1e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149; Conservative 17; Mismatches
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TISSUE=Primary B-Cells;
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Homo sapiens (Human).
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Matches 149; Conserv
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InterPro; IPR003599; IG.
InterPro; IPR003110; Ig-like.
InterPro; IPR003100; Ig C1.
InterPro; IPR003006; Ig C1.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig V.
Pfam; PP07654; C1-8et; I.
SWART; SW00407; IGC1; I.
SWART; SW00407; IGC1; I.
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.4%; Score 719.5; DB 2
69.6%; Pred. No. 6.3e-55;
ive 17; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 AA.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Interpro: IPR00110; Ig-11ke.
Interpro: IPR00110; Ig-21.
Interpro: IPR001369; Ig_C1.
Interpro: IPR001369; Ig_WHC.
Interpro: IPR001369; Ig_V.
Pfam; PP07654; C1-8et; I.
SWART; SW00407; IG21; I.
SWART; SW00406; IGV; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Glandular pool- thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC062704; AAH62704.1;
P01837; 1KCU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 69.64
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
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ઠે 셤 ઠે ò d ð 셤 SEQUENCE FROM N.A. TISSUE=Brain;

RESULT 10

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Riausner R.D., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Detchenko, L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubz R.D.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 VLTQSPGTLSLSPGERATLSCRAS--QSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWV-FGGGTKLTVLSRTVAAPSVFI
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EMBL, BC032451; AAH32451.1; -.
HSSP, P01837; 1KCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.3%; Score 717.5; DB 2
Best Local Similarity 69.6%; Pred. No. 9.4e-55;
Matches 151; Conservative 18; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                              Trausberspleen;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Attausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McZewan P.J., McKernan K.J., Malek J.A., Gunzardne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodesgren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

and mouse CDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 PSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 MTQSPSSLSASVGDRVTITCRAS---QNINNYLNWYQLKPGKAPNLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC073775, AAH73775.1;
InterPro; IPR0031599; Ig.
InterPro; IPR00710; Ig-like.
InterPro; IPR0031006; Ig-MHC.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-WHC.
InterPro; IPR003006; Ig-W.
Pfam; PF00647; Ig. 2.
SWART; SM00409; IG: 2.
SWART; SM00400; IGC; 1.
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%; Score 714.5; DB 2;
69.3%; Pred. No. 1.7e-54;
ive 16; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 TLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 69.3%
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                               SEQUENCE FROM N.A.
                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
       SOW SEE STANDING S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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KAUSTENERFERIARY B-CELIES;

RA STEAUSBESTS, PubMed=12477932; DOI=10.1073/pnas.242603899;

RA STEAUSBEST R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rodas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rodas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

RA Raha J., Helton E., Ketteman M., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Temperation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VTQE-SALTISPGETVTLICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

    Last sequence update)
    Last annotation update)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.6%; Score 709.5; DB 2 68.8%; Pred. No. 4.7e-54;
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Matches 148; Conservative 19; Mismatches
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Submitted (JUN-2004) to the EMBL/GenBankerg R.;
Submitted (JUN-2004) to the EMBL/GenBankerg EMBL;
InterPro; IPR003109; Ig.
InterPro; IPR003109; Ig.
InterPro; IPR003109; Ig.
InterPro; IPR003596; Ig. NHC.
InterPro; IPR003596; Ig. NHC.
InterPro; IPR004596; Ig. NHC.
InterPro; IPR004596; Ig. NHC.
InterPro; IPR00407; Ig. 2.
SWART; SW00407; Ig!; 2.
SWART; SW00400; IG: 2.
SWART; SW00406; IG: 2.
PR0SITE; PS00290; IG_LKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                           TISSUE=Primary B-Cells;
                                                               Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                              NCBI_TaxID=9606;
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236 AA

05-JUL-2004 (TrEMBLrel. 27, Created)

Q6GMX8; Q6GMX8 RESULT 12 Q6GMX8

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Q6PIT5
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Q6PIT5
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                                                                                                                                                                                                                                         MEDINE-22388257; PubWed=12477932; DOI=10.1073/pnas.242603899; MEDINE-22388257; PubWed=12477932; DOI=10.1073/pnas.242603899; A Grausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heish F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Gaares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S.W., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Hilalon D.K., Mullahy S.J., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., K. Townen M.M., Madan M., Schnutz J., Myers R.M., Butterfield Y.S., K. Townen M.M., Madan M., Schnutz J., Myers R.M., Butterfield Y.S., A Mones S.J., Marra M.A., A Mones S.J., Marra M.A., Touchman J.W., Green E.D., Schmerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Touchman J.W., Green E.D., Geren E.D., Schnerch A., Schein J.E., Schner A., Sche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 PSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VTOE-SALITSPGETVILICRSSIGAVITSNYANWVOEKPDHLFTGLIGGINNRAPGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 RFSGSGSGTEFSLTISGLQPDDFATYYCQPYNSNSPQFGQGTKVEI-KRTVAAPSVFIFP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25871 MW; BE01A28CD06EEE26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.3%; Score /ve.5; we e, Best Local Similarity 68.8%; Pred. No. 8.7e-54; Matches 148; Conservative 18; Mismatches 44;
                                 236 AA
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SMART; SMO0407; IG21; 1.
SMART; SMO0406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS02290; IG_MHC; UNKNOWN_1.
HYPOCHELICAL PYCLEIN
SEQUENCE 236 AA; 25871 MM; BE01A;
                                                                     Created)
                                   PRT;
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-WHC.
Pfam; PP07654; C1-set; I.
                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
                                 PRELIMINARY;
                                                                                                                   Hypothetical protein.
                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                    Q6PIH4;
                               O6PIH4
RESULT 13
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A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Rausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Holsh F.,
Rapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McEwan P.J., McKernan R.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley W.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Norley W. M. Initial analysis of more than 15,000 full-length human
M. Mandan A.M. Sminter M.J.,
R. Menneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 RCAIQLTOSPSSLSASVGERVTITCRASQG---ISSALAWYQQKPGKPPKLLIYDASTME 77
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                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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9
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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68.6%; Pred. No. 3.9e-53;
ive 15; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC29444; AAH29444.1; -.
HSSP; POIGOT; IAR2.
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236 AA; 25741 MW; BD50AF071FBEB351 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                        236
                                           202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                       236 AA
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InterPro; IPR003106; Ig-like.
InterPro; IPR003106; Ig_MC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_WC.
InterPro; IPR00407; Ig_C1.
SMART; SM00407; IGC1; 1.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00289; IG_MIC; UNKNOWN_1.
Hypothetical protein_
                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                       PRELIMINARY;
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05-JUL-2004 (TrEMBLrel
Hypothetical protein.
Homo sapiens (Human).
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Tisbulsandra (1973) pubmed=12477932; DOI=10.1073/pnas.242603899;

A REDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

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Broaks S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

Mara M.A.,

A Jones S.J., Marra M.A.,

"Manna and initial analysis of more than 15,000 full-length human
                    119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO34142; AAH34142.1; -.
HSSP; P01837; 1KBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;
                                                                   05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                   240 AA
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SMART; SM00407; IGC1; 1.
SMART; SM00406; IGC1; 1.
PROSITE; PS50835; IG LIKB; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incerpro; IPR007110; 19-11ke.
Interpro; IPR001597; 19_C1.
Interpro; IPR003597; 19_KHC.
Interpro; IPR003596; 19_MHC.
Interpro; IPR003596; 19_V.
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Matches 147; Conservative
                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Lung;
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DEQLKSGTASVVCLLANFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                   SLIGDKAALTITGAQTEDEARYFC--ALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
                                                          90 SGSGTDFTLKISRVEAEDVGVYYCMQAL-QTPPYTFGQGTKLEI-KRTVAAPSVFIFPPS 147
                                                                                                                       30 SLSVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYWGSNRASGVPDRFSG 89
                                                                                                                                                                            186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                            208 SKADYEKHKYYACEVTHQGLSSPVTKSFNRGEC 240
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Job time : 112 secs
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